

OM protein - protein search, using sw model

Run on: March 1, 2005, 08:40:57 ; Search time 13.9555 Seconds
 (without alignments)
 1690.542 Million cell updates/sec

Title: US-10-624-932-2_COPY_163_223
 Perfect score: 326
 Sequence: 1 EQGIVLPCRPPGEGIPPAEVE.....HSLVVRQARLADTANYTCVA.61

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	326	100.0	301	8	ADQ67559	Adq67559 Novel hum
2	326	100.0	330	8	ADH71620	Adh71620 Human pro
3	326	100.0	331	8	ADH71612	Adh71612 Human pro
4	326	100.0	335	8	ADH71616	Adh71616 Human pro
5	326	100.0	336	8	ADH71614	Adh71614 Human pro
6	326	100.0	817	8	ADH71624	Adh71624 Human pro
7	326	100.0	833	8	ADH71622	Adh71622 Human pro
8	326	100.0	842	5	AAU74818	Aau74818 Human REP
9	326	100.0	842	8	ADL06574	Adl06574 Human tum

10	326	100.0	898	2	AAW78898	Aaw78898	Rat	UNC-5
11	326	100.0	898	5	AAU10543	Aau10543	Rat	netri
12	326	100.0	898	5	AAU85403	Aau85403	Human	pro
13	326	100.0	898	5	AAU97899	Aau97899	Human	net
14	326	100.0	898	5	AAU97900	Aau97900	Rat	netri
15	326	100.0	898	7	ADG42580	Adg42580	Rat	trans
16	326	100.0	898	8	ADH71618	Adh71618	Human	pro
17	326	100.0	898	8	ADH71626	Adh71626	Human	pro
18	326	100.0	899	5	AAU79939	Aau79939	Human	UNC
19	326	100.0	899	7	ADG42569	Adg42569	Novel	hum
20	326	100.0	899	8	ADH71636	Adh71636	Human	pro
21	326	100.0	899	8	ADH71642	Adh71642	Human	pro
22	326	100.0	899	8	ADH71648	Adh71648	Human	pro
23	326	100.0	899	8	ADH71632	Adh71632	Human	pro
24	326	100.0	899	8	ADH71610	Adh71610	Human	pro
25	326	100.0	899	8	ADH71628	Adh71628	Human	pro
26	326	100.0	899	8	ADH71640	Adh71640	Human	pro
27	326	100.0	899	8	ADH71630	Adh71630	Human	pro
28	326	100.0	899	8	ADH71650	Adh71650	Human	pro
29	326	100.0	899	8	ADH71644	Adh71644	Human	pro
30	326	100.0	899	8	ADH71634	Adh71634	Human	pro
31	326	100.0	899	8	ADH71646	Adh71646	Human	pro
32	326	100.0	899	8	ADH71638	Adh71638	Human	pro
33	326	100.0	943	4	AAM79128	Aam79128	Human	pro
34	245	75.2	931	7	ADG42582	Adg42582	Mouse	tra
35	242	74.2	636	8	ADR99262	Adr99262	Splice	va
36	242	74.2	669	8	ADR99252	Adr99252	Human	sRO
37	242	74.2	929	7	ADG42583	Adg42583	Human	tra
38	242	74.2	931	4	AAB50691	Aab50691	Human	UNC
39	242	74.2	931	7	ADE63098	Ade63098	Human	Pro
40	242	74.2	931	7	ABU64297	Abu64297	Human	thr
41	242	74.2	931	8	ADR99258	Adr99258	Human	unc
42	242	74.2	964	8	ADR99250	Adr99250	Human	lRO
43	242	74.2	982	4	ABG11551	Abg11551	Novel	hum
44	234	71.8	931	7	ADG42584	Adg42584	Human	tra
45	230	70.6	933	5	AAO18734	Aao18734	Human	NOV

ALIGNMENTS

RESULT 1

ADQ67559

ID ADQ67559 standard; protein; 301 AA.

XX

AC ADQ67559;

XX

DT 07-OCT-2004 (first entry)

XX

DE Novel human protein sequence #2225.

XX

KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

KW gene therapy; diagnostic marker; morbid state; osteoporosis;

KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

KW cancer.

XX

OS Homo sapiens.

XX
 PN EP1440981-A2.
 XX
 PD 28-JUL-2004.
 XX
 PF 21-JAN-2004; 2004EP-00001196.
 XX
 PR 21-JAN-2003; 2003JP-00102206.
 PR 09-MAY-2003; 2003JP-00131392.
 XX
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 XX
 DR WPI; 2004-535376/52.
 DR N-PSDB; ADQ67252.
 XX
 PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 XX
 PS Claim 1; SEQ ID NO 4720; 2449pp; English.
 XX
 CC The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.
 XX
 SQ Sequence 301 AA;

Query Match 100.0%; Score 326; DB 8; Length 301;
 Best Local Similarity 100.0%; Pred. No. 1.2e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 163 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 222

 Qy 61 A 61
 |
 Db 223 A 223

RESULT 2
 ADH71620
 ID ADH71620 standard; protein; 330 AA.
 XX
 AC ADH71620;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human protein of the invention NOV21f SEQ ID NO:516.

XX
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.

PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71619.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 516; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A

CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipaemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 330 AA;

Query Match 100.0%; Score 326; DB 8; Length 330;

Best Local Similarity 100.0%; Pred. No. 1.3e-30;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPEGIPPAEVEWLRNEDLVDPNVDNVYITREHSLVVRQARLADTANYTCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 138 EQGIVLPCRPPEGIPPAEVEWLRNEDLVDPNVDNVYITREHSLVVRQARLADTANYTCV 197

Qy 61 A 61
 |
 Db 198 A 198

RESULT 3

ADH71612

ID ADH71612 standard; protein; 331 AA.

XX

AC ADH71612;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21b SEQ ID NO:508.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.

PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71611.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 508; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 331 AA;

Query Match 100.0%; Score 326; DB 8; Length 331;

Best Local Similarity 100.0%; Pred. No. 1.3e-30;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPEGIPPAEVEWLRNEDLVDPNYYITREHSLVVRQARLADTANYTCV 60
|
Db 138 EQGIVLPCRPPEGIPPAEVEWLRNEDLVDPNYYITREHSLVVRQARLADTANYTCV 197

Qy 61 A 61
|
Db 198 A 198

RESULT 4

ADH71616

ID ADH71616 standard; protein; 335 AA.

XX

AC ADH71616;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21d SEQ ID NO:512.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.

XX
 PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
 PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
 PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
 PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
 PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
 PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
 PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
 PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
 PI Zhong H;
 XX
 DR WPI; 2004-081935/08.
 DR N-PSDB; ADH71615.
 XX
 PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 21; SEQ ID NO 512; 1880pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipaemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC represents a NOVX polypeptide of the invention.
 XX
 SQ Sequence 335 AA;

Query Match 100.0%; Score 326; DB 8; Length 335;
 Best Local Similarity 100.0%; Pred. No. 1.3e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 138 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 197
 Qy 61 A 61
 |
 Db 198 A 198

RESULT 5
 ADH71614
 ID ADH71614 standard; protein; 336 AA.
 XX
 AC ADH71614;
 XX

DT 25-MAR-2004 (first entry)
XX
DE Human protein of the invention NOV21c SEQ ID NO:510.
XX
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.

PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71613.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 510; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 336 AA;

Query Match 100.0%; Score 326; DB 8; Length 336;

Best Local Similarity 100.0%; Pred. No. 1.3e-30;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 60
|
Db 141 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 200

Qy 61 A 61
|
Db 201 A 201

RESULT 6

ADH71624

ID ADH71624 standard; protein; 817 AA.

XX

AC ADH71624;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21h SEQ ID NO:520.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
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PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
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PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.

PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71623.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 520; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 817 AA;

Query Match 100.0%; Score 326; DB 8; Length 817;
Best Local Similarity 100.0%; Pred. No. 3.8e-30;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
|
Db 138 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 197

Qy 61 A 61
|
Db 198 A 198

RESULT 7

ADH71622

ID ADH71622 standard; protein; 833 AA.

XX

AC ADH71622;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21g SEQ ID NO:518.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;

KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;

KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;

KW obesity; diabetes; infectious disease; metabolic syndrome X;

KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
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PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
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PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
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PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.

PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
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PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71621.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 518; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 833 AA;

Query Match 100.0%; Score 326; DB 8; Length 833;

Best Local Similarity 100.0%; Pred. No. 3.9e-30;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy -- 1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPNVDYITREHSLVVRQARLADTANYTCV 60
|||||

Db 154 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPNVDYITREHSLVVRQARLADTANYTCV 213

Qy 61 A 61

|
Db 214 A 214

RESULT 8

AAU74818

ID AAU74818 standard; protein; 842 AA.

XX
 AC AAU74818;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Human REPTR 1 protein.
 XX
 KW REPTR; human; antiinflammatory; cytostatic; immunosuppressive; antiviral;
 KW anti-HIV; antiarthritic; anticonvulsant; nootropic; neuroprotective;
 KW antiallergic; antibody; immunogen; endometriosis;
 KW gastrointestinal disorder; gastritis; oesophageal carcinoma;
 KW Crohn's disease; irritable bowel syndrome; ulcerative colitis;
 KW endocrine disorder; hypothalamus disorder; Kallman's disease;
 KW autoimmune disease; inflammatory disease; infertility; receptor;
 KW acquired immune deficiency syndrome; AIDS; rheumatoid arthritis; allergy;
 KW osteoarthritis; diabetes mellitus; multiple sclerosis;
 KW systemic lupus erythematosus; cell proliferative disorder; cancer;
 KW developmental disorder; Duchenne muscular dystrophy;
 KW Becker muscular dystrophy; neurological disorder; epilepsy;
 KW Alzheimer's disease; Huntington's disease; reproductive disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200198354-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 21-JUN-2001; 2001WO-US019942.
 XX
 PR 21-JUN-2000; 2000US-0214027P.
 PR 25-AUG-2000; 2000US-0228045P.
 PR 12-DEC-2000; 2000US-0255104P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;
 PI Lal P, Policky JL, Azimzai Y, Lu DAM, Graul R, Yao MG, Burford N;
 PI Hafalia AJA, Baughn MR, Bandman O, Patterson C, Yang J, Xu Y;
 PI Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BM, Lu Y;
 XX
 DR WPI; 2002-090432/12.
 DR N-PSDB; ABK15169.
 XX
 PT Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful in
 PT the diagnosis, treatment and prevention of gastrointestinal (e.g.
 PT gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell
 PT proliferative (e.g. cancer) disorders.
 XX
 PS Claim 45; Page 111-113; 157pp; English.
 XX
 CC This invention relates to twelve human receptors cDNA sequences referred
 CC to as REPTR-1 to REPTR-12), and the proteins encoded thereby. The
 CC proteins of the invention may have antiinflammatory, cytostatic,
 CC immunosuppressive, antiviral, anti-HIV, antiarthritic, muscular active
 CC general, anticonvulsant, nootropic, neuroprotective, antiallergic
 CC activities. The sequences of the invention may be used to produce REPTR
 CC agonists or antagonists, and the protein sequences may be used to raise

CC anti-REPTR antibodies. These molecules and the REPTR polynucleotides and
CC polypeptides of the invention are useful in the diagnosis, treatment and
CC prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma,
CC Crohn's disease, irritable bowel syndrome, ulcerative colitis), endocrine
CC (e.g. hypothalamus disorder, Kallman's disease), autoimmune/ inflammatory
CC (e.g. acquired immune deficiency syndrome (AIDS), rheumatoid arthritis,
CC allergies, osteoarthritis, diabetes mellitus, multiple sclerosis,
CC systemic lupus erythematosus), cell proliferative (e.g. cancer),
CC developmental (e.g. Duchenne and Becker muscular dystrophy), neurological
CC (e.g. epilepsy, Alzheimer's disease, Huntington's disease) and
CC reproductive (e.g. infertility, endometriosis) disorders. Numerous other
CC examples of each disorder are given in the specification. The present
CC sequence represents the human REPTR1 protein sequence of the invention
XX
SQ Sequence 842 AA;

Query Match 100.0%; Score 326; DB 5; Length 842;
Best Local Similarity 100.0%; Pred. No. 3.9e-30;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 60
|||||
Db 163 EQGIVLPCRPPEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 222

Qy 61 A 61
|
Db 223 A 223

RESULT 9

ADL06574

ID ADL06574 standard; protein; 842 AA.

XX

AC ADL06574;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human tumour-associated antigenic target (TAT) polypeptide #73.

XX

KW Human; tumour-associated antigenic target; TAT; cell death; tumour;
KW cancer; cytostatic.

XX

OS Homo sapiens.

XX

PN WO2004016225-A2.

XX

PD 26-FEB-2004.

XX

PF 19-AUG-2003; 2003WO-US025892.

XX

PR 19-AUG-2002; 2002US-0404809P.

PR 21-AUG-2002; 2002US-0405645P.

PR 23-SEP-2002; 2002US-0413192P.

PR 15-OCT-2002; 2002US-0419008P.

PR 15-NOV-2002; 2002US-0426847P.

PR 02-JUL-2003; 2003US-0484959P.

XX

PA (GETH) GENENTECH INC.
 XX
 PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
 PI Spencer SD, Wu TD, Zhang Z;
 XX
 DR WPI; 2004-257144/24.
 DR N-PSDB; ADL06497.
 XX
 PT New antibody that binds to a tumor-associated antigenic target (TAT)
 PT polypeptide, useful for preparing a composition for diagnosing or
 PT treating cancer.
 XX
 PS Claim 2; SEQ ID NO 154; 319pp; English.
 XX
 CC The present invention relates to the isolation of human tumour-associated
 CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
 CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
 CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
 CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
 CC produced in bacteria or in CHO cells and induces death of a cell to which
 CC it binds. The antibody is useful for preparing a composition for
 CC diagnosing or treating tumours and cancer. The present sequence
 CC represents a human TAT polypeptide of the invention.
 XX
 SQ Sequence 842 AA;

Query Match 100.0%; Score 326; DB 8; Length 842;
 Best Local Similarity 100.0%; Pred. No. 3.9e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 163 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 222
 Qy 61 A 61
 |
 Db 223 A 223

RESULT 10

AAW78898

ID AAW78898 standard; protein; 898 AA.

XX

AC AAW78898;

XX

DT 25-MAR-2003 (revised)

DT 21-DEC-1998 (first entry)

XX

DE Rat UNC-5 homologue UNC5H-1.

XX

KW UNC-5; UNC5H-1; rat; netrin receptor; cell migration; axon guidance;
 KW diagnosis; therapy.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Peptide 580. .594

FT /note= "peptide used to raise rabbit polyclonal antisera"
 XX
 PN WO9837085-A1.
 XX
 PD 27-AUG-1998.
 XX
 PF 19-FEB-1998; 98WO-US003143.
 XX
 PR 19-FEB-1997; 97US-00808982.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keinomasu K;
 XX
 DR WPI; 1998-495364/42.
 DR N-PSDB; AAV52940.
 XX
 PT Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and
 PT the biopharmaceutical industry.
 XX
 PS Claim 1; Page 19-22; 32pp; English.
 XX
 CC UNC5H-1 and UNC5H-2 (see AAW78900) are rat homologues of Caenorhabditis
 CC elegans UNC-5 protein. Their amino acid sequences were deduced from
 CC isolated unc5h cDNA clones (see AAV52940 and AAV52942) isolated from an
 CC E18 brain cDNA library. The predicted proteins show similarity with UNC-
 CC 5, possess 2 predicted Ig-like domains and 2 predicted thrombospondin
 CC type-1 repeats, a predicted membrane spanning region, and a large
 CC intracellular domain. They are predicted to be involved in cell migration
 CC and axon guidance, and are characterised as receptor proteins for
 CC netrins. Human UNC5H-1 (see AAW78899) and UNC5H-2 (see AAW78901) proteins
 CC are also claimed. Vertebrate UNC-5 proteins may be produced recombinantly
 CC from transfected host cells. The invention also provides unc-5
 CC hybridisation probes and primers, vertebrate UNC-5-specific binding
 CC agents such as specific antibodies, and methods of making and using the
 CC subject compositions in diagnosis (e.g. genetic hybridisation screens for
 CC vertebrate unc-5 transcripts), therapy (e.g. gene therapy to modulate
 CC vertebrate unc-5 gene expression) and in the biopharmaceutical industry
 CC (e.g. as immunogens, reagents for modulating cell guidance, reagents for
 CC screening chemical libraries for lead pharmacological agents, etc.).
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 898 AA;

Query Match 100.0%; Score 326; DB 2; Length 898;
 Best Local Similarity 100.0%; Pred. No. 4.2e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
 |
 Db 163 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 222
 Qy 61 A 61
 |
 Db 223 A 223

RESULT 11

AAU10543

ID AAU10543 standard; protein; 898 AA.

XX

AC AAU10543;

XX

DT 14-FEB-2002 (first entry)

XX

DE Rat netrin receptor UNC5H1 (YSG7) polypeptide.

XX

KW YSG; YSG7; schizophrenia; chronic animal model; LCGU; netrin receptor;

KW local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;

KW calcium-independent alpha-latrotoxin receptor; CIRL; trkE; synapsin 1A;

KW epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic;

KW tumour necrosis factor alpha; TNF-alpha; rat.

XX

OS Rattus sp.

XX

PN WO200175440-A2.

XX

PD 11-OCT-2001.

XX

PF 02-APR-2001; 2001WO-GB001486.

XX

PR 31-MAR-2000; 2000GB-00007880.

PR 26-MAY-2000; 2000GB-00012768.

XX

PA (WELF-) WELFIDE CORP.

XX

PI Cochran S, Paterson G, Ohashi Y, Morris B, Pratt J;

XX

DR WPI; 2002-010813/01.

DR N-PSDB; AAS16843.

XX

PT Novel chronic animal model of schizophrenia, useful for identifying anti-psychotic drugs and genes that are associated with schizophrenia.

XX

PS Disclosure; Fig 8b; 79pp; English.

XX

CC The invention relates to YSG polynucleotide fragments for use in
CC diagnosing and/or developing treatments for schizophrenia using chronic
CC animal models. The polynucleotides and their encoded polypeptides are
CC used for identification of compounds which modulate the expression of YSG
CC molecules, leading to the manufacture of schizophrenia medicaments. The
CC sequences can also be used for testing candidate compounds for any effect
CC on the polypeptides. Anti-schizophrenic effects of a compound can be
CC determined by measuring local cerebral glucose utilisation (LCGU) or
CC comparing its expression level with that of a control group. The
CC sequences are useful in the identification of genes associated with
CC schizophrenic states and in the development of an antibody. The sequences
CC of the invention include phosphodiesterase 1-alpha, calcium-independent
CC alpha-latrotoxin receptors (CIRL)-1,2&3, epithelial discoidin domain
CC receptor 1 (trkE), netrin receptor (UNC5H1), synapsins 1A and AB and
CC tumour necrosis factor (TNF) alpha. This sequence represents rat netrin
CC receptor UNC5H1 (YSG7) polypeptide

XX

SQ Sequence 898 AA;

Query Match 100.0%; Score 326; DB 5; Length 898;
Best Local Similarity 100.0%; Pred. No. 4.2e-30;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     163 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 222

Qy      61 A 61
          |
Db     223 A 223
```

RESULT 12

AAU85403

ID AAU85403 standard; protein; 898 AA.

XX

AC AAU85403;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human protein NOV1.

XX

KW Human; NOVX; cardiomyopathy; atherosclerosis; diabetes;

KW cell signal processing disorder; metabolic disorder; obesity; infection;

KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; immune disorder;

KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;

KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;

KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;

KW psychosis; neurological disorder; anxiety; schizophrenia;

KW manic depression; dementia; dyskinesia; Huntington's disease;

KW Gilles de la Tourette's syndrome; gene therapy.

XX

OS Homo sapiens.

XX

PN W0200210216-A2.

XX

PD 07-FEB-2002.

XX

PF 30-JUL-2001; 2001WO-US024225.

XX

PR 28-JUL-2000; 2000US-0221409P.

PR 04-AUG-2000; 2000US-0222840P.

PR 04-AUG-2000; 2000US-0223752P.

PR 04-AUG-2000; 2000US-0223762P.

PR 04-AUG-2000; 2000US-0223769P.

PR 04-AUG-2000; 2000US-0223770P.

PR 14-AUG-2000; 2000US-0225146P.

PR 15-AUG-2000; 2000US-0225392P.

PR 15-AUG-2000; 2000US-0225470P.

PR 16-AUG-2000; 2000US-0225697P.

PR 01-FEB-2001; 2001US-0263662P.

PR 05-APR-2001; 2001US-0281645P.

XX

PA (CURA-) CURAGEN CORP.

XX
 PI Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;
 PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
 XX
 DR WPI; 2002-180074/23.
 DR N-PSDB; ABK37922.
 XX
 PT New isolated cytoplasmic, nuclear, membrane bound, or secreted
 PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
 PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
 PT immune disorders.
 XX
 PS Claim 1; Page 11; 213pp; English.
 XX
 CC The invention relates to an isolated cytoplasmic, nuclear, membrane
 CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
 CC form. Also included are the nucleic acids encoding the NOVX proteins, a
 CC vector comprising the nucleic acid, a cell comprising the vector, an anti
 CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
 CC antibody are useful for treating or preventing a NOVX-associated
 CC disorder, where the disorder is selected from cardiomyopathy,
 CC atherosclerosis, diabetes, a disorder related to cell signal processing
 CC and metabolic pathway modulation, metabolic disorders, obesity,
 CC infectious disease, anorexia, cancer-associated cachexia, cancer,
 CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
 CC immune disorders, haematopoietic disorders, and the various
 CC dyslipidaemias, metabolic disturbances associated with obesity, the
 CC metabolic syndrome X and wasting disorders associated with chronic
 CC diseases, bacterial, fungal, protozoal and viral infections, pain,
 CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
 CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
 CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
 CC hypertrophy, and psychotic and neurological disorders, including anxiety,
 CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
 CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
 CC nucleic acid is useful in gene therapy. The present sequence represents a
 CC NOVX protein
 XX
 SQ Sequence 898 AA;

Query Match 100.0%; Score 326; DB 5; Length 898;
 Best Local Similarity 100.0%; Pred. No. 4.2e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 163 EQGIVLPCRPEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCV 222
 Qy 61 A 61
 |
 Db 223 A 223

RESULT 13
 AAU97899
 ID AAU97899 standard; protein; 898 AA.
 XX

AC AAU97899;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human netrin binding membrane receptor UNC5H-1 protein.
 XX
 KW Netrin binding membrane receptor; receptor; UNC5H-1; human; nootropic;
 KW neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer;
 KW central nervous system; CNS; stroke; Parkinson's disease;
 KW multiple sclerosis; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 152. .223
 FT /note= "Immunoglobulin domain "
 FT Domain 247. .294
 FT /note= "Thrombospondine type 1 domain "
 FT Domain 302. .348
 FT /note= "Thrombospondine type 1 domain"
 FT Region 361. .382
 FT /note= "Transmembrane region"
 FT Domain 495. .598
 FT /note= "ZU5 domain"
 FT Domain 817. .897
 FT /note= "Death domain"
 XX
 PN WO200233080-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 15-OCT-2001; 2001WO-EP011891.
 XX
 PR 16-OCT-2000; 2000US-0240061P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Koehler RH;
 XX
 DR WPI; 2002-463314/49.
 DR N-PSDB; ABK52891.
 XX
 PT Novel human netrin binding membrane receptor polypeptide and
 PT polynucleotides for identifying modulating agents useful in treating
 PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
 PT Alzheimer's disease.
 XX
 PS Claim 1; Fig 2; 94pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of a novel
 CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
 CC sequence of the invention is useful as a probe for detecting a nucleic
 CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
 CC of the invention are useful to screen for agents which decrease the
 CC activity of the UNC5H-1 protein. The sequences are also useful for
 CC screening agents which regulate (modulate) the activity of the protein of
 CC the invention. A pharmaceutical composition containing the protein of the

CC invention or a reagent that modulates the activity of the UNC5H-1 protein
 CC may be useful for treating a UNC5H-1 dysfunction related disease such as
 CC cancer or a central nervous system (CNS) disorders (e.g, Parkinson's
 CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
 CC proteins comprising the UNC5H-1 protein are useful for generating
 .CC antibodies and for in various assay systems, and the protein can be used
 CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
 CC of the invention is useful for detecting a coding sequence for the UNC5H-
 CC 1 protein. The present sequence represents the human netrin binding
 CC membrane receptor UNC5H-1 protein of the invention
 XX
 SQ Sequence 898 AA;

Query Match 100.0%; Score 326; DB 5; Length 898;
 Best Local Similarity 100.0%; Pred. No. 4.2e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 60
 |
 Db 163 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 222
 Qy 61 A 61
 |
 Db 223 A 223

RESULT 14
 AAU97900

ID AAU97900 standard; protein; 898 AA.

XX

AC AAU97900;

XX

DT 27-AUG-2002 (first entry)

XX

DE Rat netrin binding membrane receptor UNC5H-1 protein.

XX

KW Netrin binding membrane receptor; receptor; UNC5H-1; Rat; nootropic;
 KW neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer;
 KW central nervous system; CNS; stroke; Parkinson's disease;
 KW multiple sclerosis; Alzheimer's disease.

XX

OS Rattus sp.

XX

FH	Key	Location/Qualifiers
FT	Domain	152. .223
FT		/note= "Immunoglobulin domain "
FT	Domain	247. .294
FT		/note= "Thrombospondine type 1 domain "
FT	Domain	302. .348
FT		/note= "Thrombospondine type 1 domain"
FT	Region	361. .382
FT		/note= "Transmembrane region"
FT	Domain	495. .598
FT		/note= "ZU5 domain"
FT	Domain	817. .897
FT		/note= "Death domain"

XX

PN WO200233080-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 15-OCT-2001; 2001WO-EP011891.
 XX
 PR 16-OCT-2000; 2000US-0240061P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Koehler RH;
 XX
 DR WPI; 2002-463314/49.
 XX
 PT Novel human netrin binding membrane receptor polypeptide and
 PT polynucleotides for identifying modulating agents useful in treating
 PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
 PT Alzheimer's disease.
 XX
 PS Disclosure; Fig 3; 94pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of a novel
 CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
 CC sequence of the invention is useful as a probe for detecting a nucleic
 CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
 CC of the invention are useful to screen for agents which decrease the
 CC activity of the UNC5H-1 protein. The sequences are also useful for
 CC screening agents which regulate (modulate) the activity of the protein of
 CC the invention. A pharmaceutical composition containing the protein of the
 CC invention or a reagent that modulates the activity of the UNC5H-1 protein
 CC may be useful for treating a UNC5H-1 dysfunction related disease such as
 CC cancer or a central nervous system (CNS) disorders (e.g, Parkinson's
 CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
 CC proteins comprising the UNC5H-1 protein are useful for generating
 CC antibodies and for in various assay systems, and the protein can be used
 CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
 CC of the invention is useful for detecting a coding sequence for the UNC5H-
 CC 1 protein. The present sequence represents the Rat netrin binding
 CC membrane receptor UNC5H-1 protein of the invention
 XX
 SQ Sequence 898 AA;

Query Match 100.0%; Score 326; DB 5; Length 898;
 Best Local Similarity 100.0%; Pred. No. 4.2e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDP SLDPNVYITREHSLVVRQARLADTANYTCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 163 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDP SLDPNVYITREHSLVVRQARLADTANYTCV 222

 Qy 61 A 61
 |
 Db 223 A 223

RESULT 15
 ADG42580

ID ADG42580 standard; protein; 898 AA.
 XX
 AC ADG42580;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Rat transmembrane receptor Unc5H1.
 XX
 KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
 KW NOVX-associated disorder; cancer; rat; transmembrane receptor; Unc5H1.
 XX
 OS Rattus norvegicus.
 XX
 PN US2003204052-A1.
 XX
 PD 30-OCT-2003.
 XX
 PF 04-OCT-2001; 2001US-00970944.
 XX
 PR 04-OCT-2000; 2000US-0237862P.
 XX
 PA (HERR/) HERRMANN J L.
 PA (RAST/) RASTELLI L.
 PA (SHIM/) SHIMKETS R A.
 XX
 PI Herrmann JL, Rastelli L, Shimkets RA;
 XX
 DR WPI; 2003-900673/82.
 XX
 PT New NOVX gene or NOVX-specific antibody, useful for preparing a
 PT composition for treating or preventing a NOVX-associated disorder, e.g.,
 PT cancer.
 XX
 PS Disclosure; SEQ ID NO 13; 118pp; English.
 XX
 CC The invention describes a new isolated polypeptide comprising: a
 CC polypeptide or its mature form comprising a sequence not given in the
 CC specification; or a variant of (A), where one or more amino acid residues
 CC in the variant differs in no more than 15% from the amino acid sequence
 CC of the mature form. The pharmaceutical composition may be administered
 CC via oral, transdermal, rectal or parenteral route. The polypeptide,
 CC nucleic acid or antibody is useful for preparing a composition for
 CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
 CC the amino acid sequence of a transmembrane receptor Unc5H1 used in a
 CC comparison with the novel human proteins of the invention.
 XX
 SQ Sequence 898 AA;

Query Match 100.0%; Score 326; DB 7; Length 898;
 Best Local Similarity 100.0%; Pred. No. 4.2e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 163 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 222
 Qy 61 A 61

Db |
 223 A 223

Search completed: March 1, 2005, 08:56:46
Job time : 14.9555 secs

OM protein - protein search, using sw model

Run on: March 1, 2005, 08:42:47 ; Search time 3.65502 Seconds
(without alignments)
1245.848 Million cell updates/sec

Title: US-10-624-932-2_COPY_163_223
Perfect score: 326
Sequence: 1 EQGIVLPCRPEGIPPAEVE.....HSLVVRQARLADTANYTCVA 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5.

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	326	100.0	898	2	US-08-808-982-5	Sequence 5, Appli
2	326	100.0	898	3	US-09-306-902A-5	Sequence 5, Appli
3	242	74.2	769	4	US-09-949-016-10665	Sequence 10665, A
4	230	70.6	943	2	US-08-808-982-7	Sequence 7, Appli
5	230	70.6	943	3	US-09-306-902A-7	Sequence 7, Appli
6	201	61.7	552	4	US-09-969-532-8	Sequence 8, Appli
7	201	61.7	563	4	US-09-969-532-6	Sequence 6, Appli
8	201	61.7	566	4	US-09-969-532-4	Sequence 4, Appli
9	201	61.7	577	4	US-09-969-532-2	Sequence 2, Appli
10	201	61.7	886	4	US-09-969-532-16	Sequence 16, Appl
11	201	61.7	897	4	US-09-969-532-14	Sequence 14, Appl

12	201	61.7	900	4	US-09-969-532-12	Sequence 12, Appl
13	201	61.7	911	4	US-09-969-532-10	Sequence 10, Appl
14	103	31.6	1209	4	US-09-130-158A-2	Sequence 2, Appli
15	94	28.8	106	2	US-08-341-843B-29	Sequence 29, Appl
16	94	28.8	106	2	US-08-427-497E-34	Sequence 34, Appl
17	94	28.8	1266	3	US-08-506-296B-4	Sequence 4, Appli
18	92.5	28.4	607	2	US-08-752-307B-12	Sequence 12, Appl
19	92.5	28.4	607	3	US-09-707-802-12	Sequence 12, Appl
20	92.5	28.4	607	3	US-09-991-326-12	Sequence 12, Appl
21	91	27.9	434	3	US-09-540-245A-19	Sequence 19, Appl
22	88.5	27.1	1461	4	US-09-976-594-531	Sequence 531, App
23	87	26.7	833	4	US-09-949-016-11496	Sequence 11496, A
24	87	26.7	1180	4	US-09-949-016-6577	Sequence 6577, Ap
25	86	26.4	1070	4	US-09-961-403-3	Sequence 3, Appli
26	82	25.2	983	3	US-09-412-554A-2	Sequence 2, Appli
27	81	24.8	1297	3	US-09-540-245A-17	Sequence 17, Appl
28	79	24.2	1651	3	US-09-540-245A-18	Sequence 18, Appl
29	78	23.9	1381	3	US-09-540-245A-16	Sequence 16, Appl
30	77.5	23.8	596	2	US-08-752-307B-13	Sequence 13, Appl
31	77.5	23.8	596	3	US-09-707-802-13	Sequence 13, Appl
32	77.5	23.8	596	3	US-09-991-326-13	Sequence 13, Appl
33	77	23.6	1395	3	US-09-540-245A-15	Sequence 15, Appl
34	76	23.3	819	4	US-09-949-016-11044	Sequence 11044, A
35	76	23.3	1018	1	US-08-408-093-6	Sequence 6, Appli
36	76	23.3	1018	1	US-08-408-420A-6	Sequence 6, Appli
37	76	23.3	1018	1	US-08-714-901-6	Sequence 6, Appli
38	76	23.3	1018	3	US-08-040-741-6	Sequence 6, Appli
39	76	23.3	1044	4	US-09-949-016-10321	Sequence 10321, A
40	75.5	23.2	112	4	US-09-858-664A-24	Sequence 24, Appl
41	75.5	23.2	112	4	US-10-274-978-25	Sequence 25, Appl
42	75.5	23.2	112	4	US-10-697-263-25	Sequence 25, Appl
43	75.5	23.2	524	4	US-09-270-767-44009	Sequence 44009, A
44	75.5	23.2	1953	4	US-09-917-254-92	Sequence 92, Appl
45	75	23.0	605	2	US-08-752-307B-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-08-808-982-5

; Sequence 5, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David

; APPLICANT: Hink, Lindsay

; APPLICANT: Masu, Masayuki

; APPLICANT: Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

```

;      ZIP: 94104
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/808,982
;      FILING DATE:
;      CLASSIFICATION: 530
;      ATTORNEY/AGENT INFORMATION:
;      NAME: OSMAN, RICHARD A
;      REGISTRATION NUMBER: 36,627
;      REFERENCE/DOCKET NUMBER: UC96-217
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (415) 343-4341
;      TELEFAX: (415) 343-4342
;      INFORMATION FOR SEQ ID NO: 5:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 898 amino acids
;      TYPE: amino acid
;      STRANDEDNESS: not relevant
;      TOPOLOGY: not relevant
;      MOLECULE TYPE: peptide
US-08-808-982-5

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Query Match          100.0%; Score 326; DB 2; Length 898;
Best Local Similarity 100.0%; Pred. No. 2.1e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      163 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 222

Qy      61 A 61
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Db      223 A 223

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RESULT 2

US-09-306-902A-5

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; Sequence 5, Application US/09306902A
; Patent No. 6277585
;      GENERAL INFORMATION:
;      APPLICANT: Tessier-Lavigne, Marc
;                  Leonárdo, E. David
;                  Hink, Lindsay
;                  Masu, Masayuki
;                  Kazuko, Keino-Masu
;      TITLE OF INVENTION: Netrin Receptors
;      NUMBER OF SEQUENCES: 9
;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;      STREET: 268 BUSH STREET, SUITE 3200
;      CITY: SAN FRANCISCO
;      STATE: CALIFORNIA
;      COUNTRY: USA

```

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;           ZIP: 94104
;   COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/306,902A
;           FILING DATE: 07-May-1999
;           CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;           NAME: OSMAN, RICHARD A
;           REGISTRATION NUMBER: 36,627
;           REFERENCE/DOCKET NUMBER: UC96-217
;   TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (415) 343-4341
;           TELEFAX: (415) 343-4342
;   INFORMATION FOR SEQ ID NO: 5:
;           SEQUENCE CHARACTERISTICS:
;           LENGTH: 898 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: not relevant
;           TOPOLOGY: not relevant
;           MOLECULE TYPE: peptide
;           SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-306-902A-5

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Query Match          100.0%;  Score 326;  DB 3;  Length 898;
Best Local Similarity 100.0%;  Pred. No. 2.1e-32;
Matches    61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy          1  EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          163 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 222

Qy          61 A 61
             |
Db          223 A 223

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RESULT 3

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US-09-949-016-10665
; Sequence 10665, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10665
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10665

Query Match 74.2%; Score 242; DB 4; Length 769;
Best Local Similarity 68.9%; Pred. No. 6.4e-22;
Matches 42; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
|| ::| ||||| |||||:||||:| | | ||| :|:|::| ||||| |||||
Db 19 EQEVLLQCRPPEGIPVAEVEWLKNEDIIDPVEDRNFYITIDHNLIQARLSDTANYTCV 78

Qy 61 A 61
|
Db 79 A 79

RESULT 4

US-08-808-982-7

; Sequence 7, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342


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; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-306-902A-7

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Query Match 70.6%; Score 230; DB 3; Length 943;
Best Local Similarity 65.5%; Pred. No. 2.7e-20;
Matches 38; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Qy 4 IVLPCRPEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCVA 61
::| |||||:| |||||:||||:| | :| :|:|:| |||||:| ||||| |
Db 168 VLLQCRPEGVPVAEVEWLKNEVDIDPAQDTNFLTIDHNLIIRQARLSDTANYTCVA 225

RESULT 6

US-09-969-532-8

; Sequence 8, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polynucleotides
Encoding the Same

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 60/237,280

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 33

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; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 8

; LENGTH: 552

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; TYPE: PRT
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; ORGANISM: homo sapiens

US-09-969-532-8

Query Match 61.7%; Score 201; DB 4; Length 552;
Best Local Similarity 58.6%; Pred. No. 6.2e-17;
Matches 34; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 4 IVLPCRPPGEGIPPAEVEWLNRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCVA 61
||| |||||:| |||||:|: |: | |: |:|:|:| |||||:|: ||||:|
Db 176 IVLHCRPPEGVPAAEVEWLKNEEPIDSEQDENIDTRADHNLIIIRQARLSDSGNYTCMA 233

RESULT 7

US-09-969-532-6

; Sequence 6, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polynucleotides
Encoding the Same

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 563
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-6

Query Match 61.7%; Score 201; DB 4; Length 563;
Best Local Similarity 58.6%; Pred. No. 6.3e-17;
Matches 34; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 4 IVLPCRPPPEGIPPAEVEWLRNEDLVDP SLDPNVYITREHSLVVRQARLADTANYTCVA 61
||| |||||:| |||||:|: :| | |: :|:|:| ||||:| ||||:|
Db 176 IVLHCRPPEGVPAAEVEWLKNEEPIDSEQDENIDTRADHNLIRQARLSDSGNYTCMA 233

RESULT 8

US-09-969-532-4

; Sequence 4, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 566
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-4

Query Match 61.7%; Score 201; DB 4; Length 566;
Best Local Similarity 58.6%; Pred. No. 6.3e-17;
Matches 34; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 4 IVLPCRPPPEGIPPAEVEWLRNEDLVDP SLDPNVYITREHSLVVRQARLADTANYTCVA 61
||| |||||:| |||||:|: :| | |: :|:|:| ||||:| ||||:|
Db 176 IVLHCRPPEGVPAAEVEWLKNEEPIDSEQDENIDTRADHNLIRQARLSDSGNYTCMA 233

RESULT 9

US-09-969-532-2

; Sequence 2, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade

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; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 577
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-2
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Query Match          61.7%; Score 201; DB 4; Length 577;
Best Local Similarity 58.6%; Pred. No. 6.5e-17;
Matches 34; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
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Qy      4 IVLPCRPPGEGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCVA 61
      ||| |||||:| |||||:|: :| | |: |:|:|:| ||||:|: ||||:|
Db      176 IVLHCRPPGVPAAEVEWLKNEEPIDSEQDENIDTRADHNLIIRQARLSDSGNYTCMA 233
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RESULT 10

US-09-969-532-16

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; Sequence 16, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 886
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-16
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Query Match          61.7%; Score 201; DB 4; Length 886;
Best Local Similarity 58.6%; Pred. No. 1.1e-16;
Matches 34; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
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Qy      4 IVLPCRPPGEGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCVA 61
      ||| |||||:| |||||:|: :| | |: |:|:|:| ||||:|: ||||:|
Db      176 IVLHCRPPGVPAAEVEWLKNEEPIDSEQDENIDTRADHNLIIRQARLSDSGNYTCMA 233
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RESULT 11

US-09-969-532-14

; Sequence 14, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 897
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-14

Query Match 61.7%; Score 201; DB 4; Length 897;
Best Local Similarity 58.6%; Pred. No. 1.1e-16;
Matches 34; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 4 IVLPCRPPEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCVA 61
||| |||||:| |||||:|: :| | |: :|:|:| ||||:|: ||||:|
Db 176 IVLHCRPPEGVPAAEVEWLKNEEPIDSEQDENIDTRADHNLIRQARLSDSGNYTCMA 233

RESULT 12

US-09-969-532-12

; Sequence 12, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 900
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-12

Query Match 61.7%; Score 201; DB 4; Length 900;
Best Local Similarity 58.6%; Pred. No. 1.1e-16;
Matches 34; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 4 IVLPCRPPEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCVA 61

Db ||| |||||:| |||||:|: :| | |: :|:|:| |||||:| ||||:|
176 IVLHCRPPEGVPAAEVEWLKNEEPIDSEQDENIDTRADHNLIIRQARLSDSGNYTCMA 233

RESULT 13

US-09-969-532-10

; Sequence 10, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 911
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-10

Query Match 61.7%; Score 201; DB 4; Length 911;
Best Local Similarity 58.6%; Pred. No. 1.1e-16;
Matches 34; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 4 IVLPCRPPGIPPAEVEWLNRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCVA 61
 ||| |||||:| |||||:|: :| | |: :|:|:| |||||:| ||||:|
Db 176 IVLHCRPPEGVPAAEVEWLKNEEPIDSEQDENIDTRADHNLIIRQARLSDSGNYTCMA 233

RESULT 14

US-09-130-158A-2

; Sequence 2, Application US/09130158A
; Patent No. 6576607
; GENERAL INFORMATION:
; APPLICANT: Schachner, Melitta
; TITLE OF INVENTION: CNS Neurite Outgrowth Modulators and
; TITLE OF INVENTION: Compositions, Cells and Method Embodying and Using Same
; FILE REFERENCE: 1094-1-001 CIP1B
; CURRENT APPLICATION NUMBER: US/09/130,158A
; CURRENT FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: US 08/636,514
; PRIOR FILING DATE: 1996-04-19
; PRIOR APPLICATION NUMBER: US 08/483,959
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/424,995
; PRIOR FILING DATE: 1995-04-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1209
; TYPE: PRT

; ORGANISM: murine
US-09-130-158A-2

Query Match 31.6%; Score 103; DB 4; Length 1209;
Best Local Similarity 37.5%; Pred. No. 0.00035;
Matches 24; Conservative 10; Mismatches 26; Indels 4; Gaps 3;

Qy 1 EQG--IVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTAN-Y 57
|:| ||||| ||:|:| : |: |:| | ||::| |: ||
Db 144 EEGDSIVLPCNPPKGLPPLHIYWM-NIELEHIEQDERVYMSQRGDLYFANVEENDSRNDY 202

Qy 58 TCVA 61
| |
Db 203 CCFA 206

RESULT 15

US-08-341-843B-29

; Sequence 29, Application US/08341843B
; Patent No. 5872225

; GENERAL INFORMATION:

; APPLICANT: Lemmon, Vance
; TITLE OF INVENTION: A Method for Characterizing the
; TITLE OF INVENTION: Nucleotide Sequence of L1CAM and
; Patent No. 5872225

; TITLE OF INVENTION: the Nucleotide Sequence
; TITLE OF INVENTION: Characterized Thereby
; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fay, Sharpe, Beall, Fagan,
; ADDRESSEE: Minnich & McKee
; STREET: 1100 Superior Avenue
; STREET: Suite 700
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2518

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; MEDIUM TYPE: storable
; COMPUTER: Compaq Prolinea 5100e
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/341,843B
; FILING DATE: No. 5872225ember 18, 1994
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/904,991
; FILING DATE: June 26, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Minnich, Richard J.
; REGISTRATION NUMBER: 24,175
; REFERENCE/DOCKET NUMBER: CWR 2 149-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (216) 861-5582
; TELEFAX: (216) 241-1666

```

;       TELEX:  (216) 980162
;  INFORMATION FOR SEQ ID NO: 29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 106
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  amino acids
;    HYPOTHETICAL:  irrelevant
;    ANTI-SENSE:  no
;    ORIGINAL SOURCE:
;      ORGANISM:  CHICKEN
;      INDIVIDUAL ISOLATE:  e9-e14 embryos brains, adult brains
;    IMMEDIATE SOURCE:
;      LIBRARY:  many lambda GT11 cDNA and genomic libraries
;      CLONE:  synthesis of 14 clones
;    PUBLICATION INFORMATION:
;      AUTHORS:  Burgoon, M.P.
;      AUTHORS:  Grumet, M.
;      AUTHORS:  Mauro, V.
;      AUTHORS:  Edelman, G.M.
;      AUTHORS:  Cunningham, B.A.
;      TITLE:  Structure of the chicken neuron-
;      TITLE:  glial cell adhesion molecule, Ng-CAM:
;      TITLE:  Origin of the polypeptides and
;      TITLE:  relation to the Ig superfamily.
;      JOURNAL:  J. Cell Biol.
;      VOLUME:  112
;      ISSUE:
;      PAGES:  1017-1029
;      DATE:  1991
US-08-341-843B-29

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Query Match          28.8%;  Score 94;  DB 2;  Length 106;
Best Local Similarity 35.9%;  Pred. No. 0.00024;
Matches   23;  Conservative   13;  Mismatches   24;  Indels    4;  Gaps    3;

Qy          1 EQG--IVLPCRPPGEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADT-ANY 57
             |:| :||| ||| |::||| |:| :| |:::| | :|: :|
Db          18 EEGDPVVLPCDPPESAVPPKIYWL-NSDIVHIAQDERVSMGQDGNLYFSNAMVGDSHPDY 76

Qy          58 TCVA 61
             ||
Db          77 ICHA 80

```

Search completed: March 1, 2005, 09:05:50
Job time : 3.65502 secs

OM protein - protein search, using sw model

Run on: March 1, 2005, 08:46:18 ; Search time 2.3813 Seconds
 (without alignments)
 2464.715 Million cell updates/sec

Title: US-10-624-932-2_COPY_163_223
 Perfect score: 326
 Sequence: 1 EQGIVLPCRPPGIPPAEVE.....HSLVVRQARLADTANYTCVA 61

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	123	37.7	919	2	T32541	unc-5 protein - Ca
2	123	37.7	947	1	B44294	unc-5 protein, lon
3	103	31.6	1209	2	T42718	probable neural ce
4	97	29.8	1450	2	A44027	165K myofibrillar
5	94	28.8	1265	1	A37967	neural cell adhesi
6	92.5	28.4	1040	2	A49356	transient axonal g
7	92.5	28.4	1040	2	A34695	axonal glycoprotei
8	91.5	28.1	26926	1	I38344	titin, cardiac mus
9	87.5	26.8	1051	2	A39712	kinase-like protei
10	87.5	26.8	5175	2	T20992	hypothetical prote
11	87.5	26.8	5198	2	T43290	hemiscentin precurs
12	86	26.4	1070	2	JC4593	protein-tyrosine k
13	85.5	26.2	7962	2	I38346	elastic titin - hu

14	84	25.8	1021	2	T42634	connectin/titin -
15	83.5	25.6	1036	2	S22383	axonin 1 precursor
16	82	25.2	773	2	T46283	hypothetical prote
17	81.5	25.0	2222	2	T13924	sdk protein - frui
18	81	24.8	423	2	T29549	hypothetical prote
19	81	24.8	1273	2	T42405	sax-3 protein - Ca
20	79.5	24.4	584	2	T08678	hypothetical prote
21	79	24.2	1612	2	T30805	duttl protein - mo
22	79	24.2	1651	2	T14160	transmembrane rece
23	78	23.9	1375	2	T13822	frazzled gene prot
24	78	23.9	1465	2	S43529	165K protein, skel
25	78	23.9	1526	2	T13823	frazzled gene prot
26	78	23.9	1880	2	T18531	tractin - medicina
27	77.5	23.8	1028	2	I58164	BIG-1 protein - ra
28	76	23.3	1018	2	A54744	contactin 1 precur
29	76	23.3	1018	2	JC4211	neural adhesion pr
30	76	23.3	1277	2	T30532	neural cell adhesi
31	75.5	23.2	1443	2	I50600	neogenin - chicken
32	75.5	23.2	1896	2	T08851	Down syndrome cell
33	75	23.0	1020	2	S05944	neuronal cell surf
34	75	23.0	1021	2	A57112	contactin precurso
35	75	23.0	1091	2	S01998	contactin precurso
36	75	23.0	1259	2	A43425	Bravo/Nr-CAM cell
37	74.5	22.9	761	1	IJHUNG	neural cell adhesi
38	74.5	22.9	811	2	A41054	fasciclin II, tran
39	74.5	22.9	873	2	B41054	fasciclin II PI-li
40	74.5	22.9	1197	2	T30581	neural cell adhesi
41	74.5	22.9	1232	2	T43027	neural cell adhesi
42	74	22.7	1033	2	S19247	cell adhesion prot
43	74	22.7	1239	1	A32579	neuroglian - fruit
44	74	22.7	1260	1	S05479	neural cell adhesi
45	74	22.7	1268	1	A39640	neural cell adhesi

ALIGNMENTS

RESULT 1

T32541

unc-5 protein - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T32541

R;Latreille, P.

submitted to the EMBL Data Library, December 1997

A;Description: The sequence of *C. elegans* cosmid B0273.

A;Reference number: Z21187

A;Accession: T32541

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-919 <LAT>

A;Cross-references: UNIPROT:O44171; EMBL:AF036698; PIDN:AAB88355.1;

GSPDB:GN00022; CESP:B0273.4a

A;Experimental source: strain Bristol N2; clone B0273

C;Genetics:

A;Gene: unc-5; CESP:B0273.4a

A;Map position: 4

A;Introns: 41/3; 108/1; 142/3; 201/1; 323/2; 553/1; 858/3
C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology;
thrombospondin type 1 repeat homology

Query Match 37.7%; Score 123; DB 2; Length 919;
Best Local Similarity 44.6%; Pred. No. 3.8e-06;
Matches 25; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

Qy 6 LPCRPPEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCVA 61
|||: || | ||: | :: :| | | || : ||:: |||:|: |||| |
Db 130 LPCQAPESDPKAELTWYKDGVVVQP--DANVIRASDGLIMSAARLSDSGNYTCEA 183

RESULT 2

B44294

unc-5 protein, long form - *Caenorhabditis elegans*

N;Contains: unc-5 protein, short form

C;Species: *Caenorhabditis elegans*

C;Date: 30-Apr-1993 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004

C;Accession: B44294; T32540; A44294

R;Leung-Hagesteijn, C.; Spence, A.M.; Stern, B.D.; Zhou, Y.; Su, M.W.;

Hedgecock, E.M.; Culotti, J.G.

Cell 71, 289-299, 1992

A;Title: UNC-5, a transmembrane protein with immunoglobulin and thrombospondin type 1 domains, guides cell and pioneer axon migrations in *C. elegans*.

A;Reference number: A44294; MUID:93046629; PMID:1384987

A;Contents: variety Bergerac

A;Accession: B44294

A;Molecule type: DNA

A;Residues: 1-947 <LEU>

A;Cross-references: UNIPROT:O44171; GB:S47168; NID:g258527; PIDN:AAB23867.1; PID:g258529

A;Note: sequence extracted from NCBI backbone (NCBIN:116668, NCBIN:116670, NCBIN:116672, NCBIN:116674, NCBIN:116676, NCBIN:116678, NCBIN:116680, NCBIN:116682, NCBIN:116685, NCBIP:118648)

A;Note: authors translated the codon CTA for residue 642 as Val; sequence shown follows the authors' translation

A;Note: mRNA lacking the first exon is equally prevalent

R;Latreille, P.

submitted to the EMBL Data Library, December 1997

A;Description: The sequence of *C. elegans* cosmid B0273.

A;Reference number: Z21187

A;Accession: T32540

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-947 <LAT>

A;Cross-references: EMBL:AF036698; PIDN:AAB88356.1; GSPDB:GN00022; CESP:B0273.4b

A;Experimental source: strain Bristol N2; clone B0273

C;Genetics:

A;Gene: unc-5

A;Map position: 4

A;Introns: 28/1; 69/3; 136/1; 170/3; 229/1; 351/2; 581/1; 886/3

C;Function:

A;Description: required for guidance of pioneering axons and cells migrating dorsally along the body wall; proposed to be a receptor on the surface of the motile cells

C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology;
 thrombospondin type 1 repeat homology
 C;Keywords: alternative splicing; duplication; glycoprotein; receptor;
 transmembrane protein
 F;30-947/Product: unc-5 protein, short form #status predicted <ALT>
 F;46-116/Domain: immunoglobulin homology <IM1>
 F;153-211/Domain: immunoglobulin homology <IM2>
 F;229-300/Domain: thrombospondin type 1 repeat homology #status atypical <THR1>
 F;301-354/Domain: thrombospondin type 1 repeat homology <THR2>
 F;365-390/Domain: transmembrane #status predicted <TMM>
 F;512-559/Domain: SH3 homology <SH3>
 F;53-114,65-112,160-209/Disulfide bonds: #status predicted
 F;206/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.7%; Score 123; DB 1; Length 947;
 Best Local Similarity 44.6%; Pred. No. 4e-06;
 Matches 25; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

Qy 6 LPCRPPEGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCVA 61
 |||: || | ||: | :: :| | | || : ||:: |||:|: |||| |
 Db 158 LPCQAPESDPKAELTWYKDGWVVP--DANVIRASDGSILMSAARLSDSGNYTCEA 211

RESULT 3

T42718

probable neural cell adhesion molecule L1 precursor - mouse

N;Alternate names: CHL1 protein

C;Species: Mus musculus (house mouse)

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C;Accession: T42718

R;Holm, J.; Hillenbrand, R.; Steuber, V.; Bartsch, U.; Moos, M.; Luebbert, H.;
 Montag, D.; Schachner, M.

submitted to the EMBL Data Library, December 1995

A;Description: Structural features of a close homolog of L1 (CHL1) in the mouse:
 a novel member of the L1 family of neural recognition molecules.

A;Reference number: Z22239

A;Accession: T42718

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1209 <HOL>

A;Cross-references: UNIPROT:P70232; EMBL:X94310; PIDN:CAA63972.1

A;Experimental source: brain

C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat
 homology; immunoglobulin homology

C;Keywords: cell adhesion; duplication; glycoprotein; transmembrane protein

Query Match 31.6%; Score 103; DB 2; Length 1209;
 Best Local Similarity 37.5%; Pred. No. 0.0011;
 Matches 24; Conservative 10; Mismatches 26; Indels 4; Gaps 3;

Qy 1 EQG--IVLPCRPEGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTAN-Y 57
 |:| ||||| ||:|:| | : |:| :| | ||::: | |:| |
 Db 144 EEGDSIVLPCNPPKGLPPLHIYWM-NIELEHIEQDERVYMSQRGDLYFANVEENDSRNDY 202
 Qy 58 TCVA 61
 | |
 Db 203 CCFA 206

RESULT 4

A44027

165K myofibrillar M-band structural protein - chicken

C;Species: Gallus gallus (chicken)

C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A44027

R;Noguchi, J.; Yanagisawa, M.; Imamura, M.; Kasuya, Y.; Sakurai, T.; Tanaka, T.; Masaki, T.

J. Biol. Chem. 267, 20302-20310, 1992

A;Title: Complete primary structure and tissue expression of chicken pectoralis M-protein.

A;Reference number: A44027; MUID:93015907; PMID:1400348

A;Accession: A44027

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-1450 <NOG>

A;Cross-references: UNIPROT:Q02173; GB:D11474; NID:g222832; PIDN:BAA02033.1; PID:g222833

A;Experimental source: pectoralis muscle

A;Note: sequence extracted from NCBI backbone (NCBIN:115719, NCBIP:115720)

C;Superfamily: skelemin

Query Match 29.8%; Score 97; DB 2; Length 1450;
Best Local Similarity 34.5%; Pred. No. 0.0067;
Matches 20; Conservative 10; Mismatches 24; Indels 4; Gaps 1;

Qy 8 CRPPEGIPPAEVEWLRNEDLVDPSPVNYITRE----HSLVVRQARLADTANYTCVA 61
| :| | |:| :||:|: |: || | | : :| |:| |: ||
Db 162 CFTVQGFSPVWQWYKNEELITPASDPAKYSVENKYGVHVLHINRADFDSDSATYSAVA 219

RESULT 5

A37967

neural cell adhesion molecule Ng-CAM precursor - chicken

N;Alternate names: neural glycoprotein G4

C;Species: Gallus gallus (chicken)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A37967; A60850; S16452

R;Burgoon, M.P.; Grumet, M.; Mauro, V.; Edelman, G.M.; Cunningham, B.A.

J. Cell Biol. 112, 1017-1029, 1991

A;Title: Structure of the chicken neuron-glia cell adhesion molecule, Ng-CAM: origin of the polypeptides and relation to the Ig superfamily.

A;Reference number: A37967; MUID:91154306; PMID:1705558

A;Accession: A37967

A;Molecule type: mRNA

A;Residues: 1-1265 <BUR>

A;Cross-references: GB:X56969

R;Rathjen, F.G.; Wolff, J.M.; Frank, R.; Bonhoeffer, F.; Rutishauser, U.

J. Cell Biol. 104, 343-353, 1987

A;Title: Membrane glycoproteins involved in neurite fasciculation.

A;Reference number: A60850; MUID:87109457; PMID:3805123

A;Accession: A60850

A;Molecule type: protein

A;Residues: 21-29, 'X', 31-37 <RAT>

C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; immunoglobulin homology
 C;Keywords: cell adhesion; duplication; glycoprotein; membrane protein
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-1265/Product: neural cell adhesion molecule Ng-CAM #status predicted <MAT>
 F;340-398/Domain: immunoglobulin homology <IMM1>
 F;433-491/Domain: immunoglobulin homology <IMM2>
 F;524-582/Domain: immunoglobulin homology <IMM3>

Query Match 28.8%; Score 94; DB 1; Length 1265;
 Best Local Similarity 35.9%; Pred. No. 0.013;
 Matches 23; Conservative 13; Mismatches 24; Indels 4; Gaps 3;

Qy 1 EQG--IVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADT-ANY 57
 |:| :||| ||| |::||| |:| :| |:::| | :|: :|
 Db 144 EEGDPVVLPCDPPEASAVPPKIYWL-NSDIVHIAQDERVSMGQDGNLYFSNAMVGDSHPDY 202
 Qy 58 TCVA 61
 | |
 Db 203 ICHA 206

RESULT 6

A49356

transient axonal glycoprotein TAG-1 precursor - human

N;Alternate names: axonin-1

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004

C;Accession: S35508; S28830; A49356

R;Hasler, T.

submitted to the EMBL Data Library, September 1992

A;Reference number: S35508

A;Accession: S35508

A;Molecule type: mRNA

A;Residues: 1-1040 <HAS>

A;Cross-references: UNIPROT:Q02246; EMBL:X68274; NID:g36674; PIDN:CAA48335.1; PID:g36675

R;Hasler, T.H.; Rader, C.; Stoeckli, E.T.; Zuellig, R.A.; Sonderegger, P.
 Eur. J. Biochem. 211, 329-339, 1993

A;Title: cDNA cloning, structural features, and eucaryotic expression of human TAG-1/axonin-1.

A;Reference number: S28830; MUID:93145965; PMID:8425542

A;Accession: S28830

A;Molecule type: mRNA

A;Residues: 1-296,'T',298-1040 <HA2>

A;Cross-references: EMBL:X68274

R;Tsiotra, P.C.; Karagogeos, D.; Theodorakis, K.; Michaelidis, T.M.; Modi, W.S.; Furley, A.J.; Jessell, T.M.; Papamatheakis, J.
 Genomics 18, 562-567, 1993

A;Title: Isolation of the cDNA and chromosomal localization of the gene (TAX1) encoding the human axonal glycoprotein TAG-1.

A;Reference number: A49356; MUID:94140354; PMID:8307567

A;Accession: A49356

A;Molecule type: mRNA

A;Residues: 1-1001,'G',1003-1040 <TSI>

A;Cross-references: GB:X67734

C;Genetics:

Qy 51 LADTANYTCVA 61
 :| ||:|:|
Db 202 -SDLGNYSCIA 211

RESULT 8

I38344

titin, cardiac muscle [validated] - human

N;Alternate names: connectin

N;Contains: serine/threonine-specific protein kinase (EC 2.7.1.-)

C;Species: Homo sapiens (man)

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004

C;Accession: I38344; I38345; S20898; S20897; S20899; S63665; S37393

R;Labeit, S.; Kolmerer, B.

Science 270, 293-296, 1995

A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.

A;Reference number: A57430; MUID:96026330; PMID:7569978

A;Accession: I38344

A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-26926 <LAB1>

A;Cross-references: UNIPROT:Q10466; EMBL:X90568; NID:g1017424; PID:g1017425

R;Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A.

Biochemistry 34, 553-561, 1995

A;Title: Dissecting titin into its structural motifs: identification of an alpha-helix motif near the titin N-terminus.

A;Reference number: I38345; MUID:95119041; PMID:7819249

A;Accession: I38345

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1977-2014 <MUS>

A;Cross-references: EMBL:X83270; NID:g602579; PIDN:CAA58243.1; PID:g602580

A;Note: conformation and properties are reported for a synthetic peptide corresponding to the translated fragment shown

R;Labeit, S.; Gautel, M.; Lakey, A.; Trinick, J.

EMBO J. 11, 1711-1716, 1992

A;Title: Towards a molecular understanding of titin.

A;Reference number: S20897; MUID:92258380; PMID:1582406

A;Accession: S20898

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 13597-14200,'I',14202-14696 <LAB2>

A;Cross-references: EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193

A;Accession: S20897

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 16330-16382,'S',16384-16756,'F',16758-16860 <LAB3>

A;Cross-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191

A;Accession: S20899

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 'P',22278-22431,'R',22433-22448,'G',22450-22453,'Q',22455-

22480,'TR',22483-22669,'N',22671-22696,'SA',22699-23323,'L',23325-25376 <LAB4>

A;Cross-references: EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195

R;Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.; Labeit, S.

J. Mol. Biol. 256, 556-563, 1996
A;Title: Genomic organization of M line titin and its tissue-specific expression in two distinct isoforms.
A;Reference number: S63665; MUID:96177761; PMID:8604138
A;Accession: S63665
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 26729-26825 <KOL>
A;Cross-references: EMBL:X92412; NID:gl236761
R;Gautel, M.; Leonard, K.; Labeit, S.
EMBO J. 12, 3827-3834, 1993
A;Title: Phosphorylation of KSP motifs in the C-terminal region of titin in differentiating myoblasts.
A;Reference number: S37393; MUID:94008990; PMID:8404852
A;Accession: S37393
A;Molecule type: mRNA
A;Residues: 26831-26926 <GAU>
R;Improt, S.; Politou, A.S.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, February 1996
A;Reference number: A66736; PDB:1TIT
A;Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
R;Pfuhl, M.; Pastore, A.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A66201; PDB:1NCT
A;Contents: annotation; conformation by (1)H-NMR, residues 'S',26059-26155
C;Genetics:
A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q32
C;Function:
A;Description: structural protein forming filaments in striated muscle
C;Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology; protein kinase homology
C;Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; glycoprotein; heart; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase; skeletal muscle; structural protein
F;24752-25008/Domain: protein kinase homology <KIN>
F;84,177,905,2276,2378,2459,2481,2563,2669,2763,2896,3088,3179,3384,3432,3628,3772,4068,4318,5047,5246,5823,6213,6264,6699,6800,7083,7300,7506,7597,8338,8447,8455,8719,8938,9375,10130,10133,10177,10398,11066,11488,11515,11635,11949,12170,12478,12526,12645,12875,13001,13036,13295,13540,13787,13986,14085,14529,14870,14910,15438,15704,16397,16520,16695/Binding site: carbohydrate (Asn) (covalent)
#status predicted
F;16780,16976,17579,17602,17667,17681,17845,17899,18121,18188,18209,18336,18670,18680,18685,18707,18945,19198,19238,19346,19753,19786,20034,20056,20183,20324,20426,20840,21270,21407,21538,21566,21665,21900,21935,22295,22495,22627,22897,23024,23318,23883,24012,24177,24290,24447,24642,24840,25201,25927,26133,26283,26682,26698,26811/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;26171,26178,26184,26190/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 28.1%; Score 91.5; DB 1; Length 26926;
Best Local Similarity 38.0%; Pred. No. 0.79;
Matches 19; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

Qy 13 GIPPAEVEWLRNEDLVDPSPDPN-VYITREHSLVVRQARLADTANYTCVA 61
||| ::| | |: || | |: :|||: :| | |||:

RESULT 9

A39712

kinase-like protein klg precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 09-Jul-2004

C;Accession: A39712

R;Chou, Y.H.; Hayman, M.J.

Proc. Natl. Acad. Sci. U.S.A. 88, 4897-4901, 1991

A;Title: Characterization of a member of the immunoglobulin gene superfamily that possibly represents an additional class of growth factor receptor.

A;Reference number: A39712; MUID:91271300; PMID:1711213

A;Accession: A39712

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1051 <CHO>

A;Cross-references: UNIPROT:Q91048; GB:M63437; NID:g212235; PIDN:AAA48933.1; PID:g212236

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology

C;Keywords: ATP

F;775-1046/Domain: protein kinase homology <KIN>

F;783-791/Region: protein kinase ATP-binding motif

Query Match 26.8%; Score 87.5; DB 2; Length 1051;
Best Local Similarity 35.3%; Pred. No. 0.06;
Matches 18; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

Qy 12 EGIPPAEVEWLRNEDLVDPs-LDPNVYITREHSLVVRQARLADTANYTCVA 61
||| :| : :||| | | : | ||| : | : ||| :|
Db 597 EGDVPVPHIQWKGKDKILDPSKLLPRIQIMPNGSLVIYDVTTEDSGKYTCIA 647

RESULT 10

T20992

hypothetical protein F15G9.4a - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T20992; T24733

R;Sulston, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19355

A;Accession: T20992

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5175 <WIL>

A;Cross-references: UNIPROT:Q8I0L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a

A;Experimental source: clone F15G9

R;Kershaw, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19929

A;Accession: T24733

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5175 <WI2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: CESP:F15G9.4a
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3;
1184/3; 1225/3; 1486/3; 1516/3; 1546/1; 1607/3; 1642/1; 1680/3; 1717/1; 1784/2;
1837/3; 1867/3; 2188/1; 2255/2; 2382/1; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1;
2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 3083/3; 3125/1; 3149/3; 3193/2;
3215/1; 3258/1; 3597/2; 3665/1; 3722/3; 3764/1; 3810/1; 3857/1; 4043/1; 4187/1;
4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1;
5077/1; 5110/1

RESULT 11

hemicentin precursor - *Caenorhabditis elegans*

C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 09-Jul-2004

R; Vogel, B.E.; Hedgecock, E.M.

A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-line chromosome segregation in *C. elegans*.

A;Accession: T43290

A;Molecule type: mRNA

A;Cross-references: UNIPROT:O76518; EMBL:AF074901; PIDN:AAC26792.1

submitted to the EMBL Data Library, December 1994

A;Accession: T20993

A;Molecule type: DNA

A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b

R;Kershaw, J.

A;Reference number: Z19929

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-5198 <WI2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: him-4; F15G9.4b
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3;
1184/3; 1225/3; 1486/3; 1516/3; 1546/1; 1607/3; 1642/1; 1680/3; 1717/1; 1784/2;
1837/3; 1867/3; 2188/1; 2255/2; 2382/1; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1;
2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 3083/3; 3125/1; 3149/3; 3193/2;
3215/1; 3258/1; 3597/2; 3665/1; 3722/3; 3764/1; 3810/1; 3857/1; 4043/1; 4187/1;
4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1;
5100/1; 5133/

RESULT 12

protein-tyrosine kinase-related receptor PTK7 precursor - human
N;Alternate names: receptor protein tyrosine kinase-like protein (RPTK)
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1996 #sequence_revision 24-May-1996 #text_change 16-Aug-2004
C;Accession: JC4593
R;Park, S.K.; Lee, H.S.; Lee, S.T.
J. Biochem. 119, 235-239, 1996
A;Title: Characterization of the human full-length PTK7 cDNA encoding a receptor
protein tyrosine kinase-like molecule closely related to chick KLG.
A;Reference number: JC4593; MUID:97037064; PMID:8882711
A;Accession: JC4593
A;Molecule type: mRNA
A;Residues: 1-1070 <PAR>
A;Cross-references: GB:U40271; NID:g1322231; PIDN:AAC50484.1; PID:g1322232
C;Comment: This protein is a member of receptor protein tyrosine kinase family,
but probably lacks the catalytic activity of tyrosine kinase. This protein
functions as a cell adhesion molecule.
C;Genetics:
A;Gene: GDB:PTK7
A;Cross-references: GDB:134760; OMIM:601890
A;Map position: 6p21.1-6p12.2
C;Superfamily: protein kinase homology
C;Keywords: cell adhesion; extracellular protein; glycoprotein;
phosphotransferase; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-1070/Product: protein-tyrosine kinase 7 #status predicted <MAT>
F;31-703/Domain: extracellular #status predicted <EXC>

F;704-725/Domain: transmembrane #status predicted <TMM>
F;726-1070/Domain: intracellular #status predicted <INC>
F;794-1065/Domain: protein kinase homology <KIN>
F;116,175,184,214,268,283,405,463,567,646/Binding site: carbohydrate (Asn)
(covalent) #status predicted

Query Match 26.4%; Score 86; DB 2; Length 1070;
Best Local Similarity 31.0%; Pred. No. 0.091;
Matches 18; Conservative 14; Mismatches 24; Indels 2; Gaps 2;

Qy 5 VLPCRPPGEGIPPAEVEWLRNEDLVDPs-LDPNVYITREHSLVVRQARLADTANYTCVA 61
:| | :| | :| : :||: | | :| : |||: | : |||:
Db 610 LLQCE-AQGDPKPLIQWKGKDRILDPTKLGPRMHIFQNGSLVIHDVAPEDSGRYTCIA 666

RESULT 13

I38346

elastic titin - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C;Accession: I38346

R;Labeit, S.; Kolmerer, B.

Science 270, 293-296, 1995

A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.

A;Reference number: A57430; MUID:96026330; PMID:7569978

A;Accession: I38346

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-7962 <RES>

A;Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427

C;Genetics:

A;Gene: GDB:TTN

A;Cross-references: GDB:127867; OMIM:188840

A;Map position: 2q31-2q31

Query Match 26.2%; Score 85.5; DB 2; Length 7962;
Best Local Similarity 36.5%; Pred. No. 1;
Matches 19; Conservative 9; Mismatches 19; Indels 5; Gaps 2;

Qy 13 GIPPAEVEWLRNEDLVDPsLDPNVYITREHSLVVRQARLAD---TANYTCVA 61
| || : ||::: :| | |||: | : | | | : ||| |
Db 1738 GSPPISITWLKDDQILDE--DDNVYISFVDSVATLQIRSVDNHSGRYTCQA 1787

RESULT 14

T42634

connectin/titin - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C;Accession: T42634

R;Yajima, H.; Ohtsuka, H.; Kume, H.; Endo, T.; Kimura, S.; Maruyama, K.
Zool. Sci. 13, 119-123, 1996

A;Title: Molecular cloning of a partial cDNA clone encoding the C terminal region of chicken breast muscle connectin.

A;Reference number: Z22220; MUID:96261234; PMID:8688806

A;Accession: T42634
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-1021 <YAJ>
 A;Cross-references: UNIPROT:P79757; EMBL:D83008; NID:g1181556; PIDN:BAA11678.1;
 PID:g1777308
 A;Experimental source: breast muscle; clone CC4
 C;Keywords: skeletal muscle

Query Match 25.8%; Score 84; DB 2; Length 1021;
 Best Local Similarity 34.9%; Pred. No. 0.15;
 Matches 22; Conservative 11; Mismatches 24; Indels 6; Gaps 3;

Qy. 2 QGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDNVYITRE---HSLVVRQARLADTANYT 58
 | :: | | | ||||| : :: :: || :|| :| | ::|| ||
 Db 749 QDVLFTCE-VSGDPSPEVEWLRNNQPI--AVSSHMRATRSKNTYSLEIRNAAVSDTGKYT 805
 Qy 59 CVA 61
 |
 Db 806 VKA 808

RESULT 15

S22383

axonin 1 precursor - chicken

N;Alternate names: neural cell adhesion molecule AxCAM

C;Species: Gallus gallus (chicken)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: S22383; S34107; S69332; S22128

R;Zuellig, R.A.; Rader, C.; Schroeder, A.; Kalousek, M.B.; von Bohlen und Halbach, F.; Osterwalder, T.; Inan, C.; Stoeckli, E.T.; Affolter, H.U.; Fritz, A.; Hafen, E.; Sonderegger, P.

Eur. J. Biochem. 204, 453-463, 1992

A;Title: The axonally secreted cell adhesion molecule, axonin-1. Primary structure, immunoglobulin-like and fibronectin-type-III-like domains and glycosyl-phosphatidylinositol anchorage.

A;Reference number: S22383; MUID:92174898; PMID:1311675

A;Accession: S22383

A;Molecule type: mRNA

A;Residues: 1-1036 <ZUE1>

A;Cross-references: UNIPROT:P28685; EMBL:X63101; NID:g62852; PIDN:CAA44815.1; PID:g62853

A;Accession: S34107

A;Molecule type: protein

A;Residues: 29-49;51-80;84-95;100-117;120-128;130-141;143-176;243-254;256-296;303-336;338-356;358-400;421-449;477-500;502-512;549-588;594-671;675-726;737-762;772-780;825-834;880-901;936-980 <ZUE2>

R;Giger, R.J.; Vogt, L.; Zuellig, R.A.; Rader, C.; Hennehan-Beatty, A.; Wolfer, D.P.; Sonderegger, P.

Eur. J. Biochem. 227, 617-628, 1995

A;Title: The gene of chicken axonin-1. Complete structure and analysis of the promoter.

A;Reference number: S69332; MUID:95172044; PMID:7867620

A;Accession: S69332

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1002-1036 <GIG>

A;Cross-references: EMBL:X79607

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994

C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology

C;Keywords: cell adhesion

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-1036/Product: axonin 1 #status predicted <MAT>

F;336-392/Domain: immunoglobulin homology <IMM>

Query Match 25.6%; Score 83.5; DB 2; Length 1036;

Best Local Similarity 31.0%; Pred. No. 0.17;

Matches 18; Conservative 13; Mismatches 24; Indels 3; Gaps 2;

Qy 4 IVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVA 61

:::|: | | | : |: | | | : |:| :| || |

Db 431 VIIPCQ-PRAAPKATVLWTKGTELLTNS--SRVTITADGTLILQNISKSDGKYTCFA 485

Search completed: March 1, 2005, 09:07:19

Job time : 3.3813 secs

OM protein - protein search, using sw model

Run on: March 1, 2005, 09:06:01 ; Search time 11.7404 Seconds
(without alignments)
1704.439 Million cell updates/sec

Title: US-10-624-932-2_COPY_163_223
Perfect score: 326
Sequence: 1 EQGIVLPCRPEGIPPAEVE.....HSLVVRQARLADTANYTCVA 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	326	100.0	842	15	US-10-311-623-1	Sequence 1, Appli
2	326	100.0	898	10	US-09-933-261-5	Sequence 5, Appli
3	326	100.0	898	10	US-09-918-779-2	Sequence 2, Appli
4	326	100.0	898	10	US-09-970-944-13	Sequence 13, Appl
5	326	100.0	898	14	US-10-256-702-5	Sequence 5, Appli
6	326	100.0	898	14	US-10-240-154-16	Sequence 16, Appl
7	326	100.0	898	15	US-10-624-932-2	Sequence 2, Appli
8	326	100.0	899	10	US-09-970-944-2	Sequence 2, Appli
9	245	75.2	931	10	US-09-970-944-15	Sequence 15, Appl
10	245	75.2	931	11	US-09-972-211-121	Sequence 121, App
11	245	75.2	931	15	US-10-087-684-35	Sequence 35, Appl
12	245	75.2	931	15	US-10-037-417-117	Sequence 117, App
13	245	75.2	931	15	US-10-096-625-121	Sequence 121, App
14	245	75.2	1010	15	US-10-218-779-35	Sequence 35, Appl
15	242	74.2	931	10	US-09-970-944-16	Sequence 16, Appl
16	242	74.2	931	10	US-09-970-944-17	Sequence 17, Appl
17	242	74.2	931	11	US-09-972-211-122	Sequence 122, App
18	242	74.2	931	11	US-09-972-211-125	Sequence 125, App
19	242	74.2	931	15	US-10-087-684-36	Sequence 36, Appl
20	242	74.2	931	15	US-10-218-779-36	Sequence 36, Appl
21	242	74.2	931	15	US-10-037-417-118	Sequence 118, App
22	242	74.2	931	15	US-10-037-417-119	Sequence 119, App
23	242	74.2	931	15	US-10-037-417-120	Sequence 120, App
24	242	74.2	931	15	US-10-096-625-122	Sequence 122, App
25	242	74.2	931	15	US-10-096-625-125	Sequence 125, App
26	230	70.6	933	15	US-10-087-684-2	Sequence 2, Appli
27	230	70.6	933	15	US-10-087-684-4	Sequence 4, Appli
28	230	70.6	933	15	US-10-218-779-2	Sequence 2, Appli
29	230	70.6	933	15	US-10-218-779-4	Sequence 4, Appli
30	230	70.6	943	10	US-09-933-261-7	Sequence 7, Appli
31	230	70.6	943	14	US-10-256-702-7	Sequence 7, Appli
32	230	70.6	945	11	US-09-972-211-123	Sequence 123, App
33	230	70.6	945	11	US-09-972-211-124	Sequence 124, App
34	230	70.6	945	14	US-10-028-072-146	Sequence 146, App
35	230	70.6	945	14	US-10-140-808-146	Sequence 146, App
36	230	70.6	945	14	US-10-121-049-146	Sequence 146, App
37	230	70.6	945	14	US-10-123-904-146	Sequence 146, App
38	230	70.6	945	14	US-10-140-470-146	Sequence 146, App
39	230	70.6	945	14	US-10-175-746-146	Sequence 146, App
40	230	70.6	945	14	US-10-176-918-146	Sequence 146, App
41	230	70.6	945	14	US-10-176-921-146	Sequence 146, App
42	230	70.6	945	14	US-10-137-865-146	Sequence 146, App
43	230	70.6	945	14	US-10-140-474-146	Sequence 146, App
44	230	70.6	945	14	US-10-142-431-146	Sequence 146, App
45	230	70.6	945	14	US-10-143-114-146	Sequence 146, App

ALIGNMENTS

RESULT 1

US-10-311-623-1

; Sequence 1, Application US/10311623

; Publication No. US20040023244A1

```

; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Danniel B.
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; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 842
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CD1
US-10-311-623-1

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Query Match          100.0%; Score 326; DB 15; Length 842;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches    61; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      163 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCV 222

Qy      61 A 61
          |
Db      223 A 223

```

```

RESULT 2
US-09-933-261-5
; Sequence 5, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
;   APPLICANT: Tessier-Lavigne, Marc
;   Leonardo, E. David

```

```

;           Hink, Lindsay
;           Masu, Masayuki
;           Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;     STREET: 268 BUSH STREET, SUITE 3200
;     CITY: SAN FRANCISCO
;     STATE: CALIFORNIA
;     COUNTRY: USA
;     ZIP: 94104
; COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/933,261
;     FILING DATE: 20-Aug-2001
;     CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/808,982
;     FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;     NAME: OSMAN, RICHARD A
;     REGISTRATION NUMBER: 36,627
;     REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 343-4341
;     TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 5:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 898 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: No. US20030040046A1 Relevant
;         TOPOLOGY: No. US20030040046A1 Relevant
;     MOLECULE TYPE: peptide
;     SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-933-261-5

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Query Match          100.0%;  Score 326;  DB 10;  Length 898;
Best Local Similarity 100.0%;  Pred. No. 1.1e-29;
Matches    61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy      1  EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      163 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 222

Qy      61 A 61
          |
Db      223 A 223

```

```

RESULT 3
US-09-918-779-2
; Sequence 2, Application US/09918779

```

; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennnda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-779-2

Query Match 100.0%; Score 326; DB 10; Length 898;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     163 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 222

Qy      61 A 61
      |
Db     223 A 223
```

RESULT 4

US-09-970-944-13

; Sequence 13, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-970-944-13

Query Match 100.0%; Score 326; DB 10; Length 898;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     163 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 222

Qy      61 A 61
      |
Db     223 A 223
```

RESULT 5

US-10-256-702-5

; Sequence 5, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David

```

;           Hink, Lindsay
;           Masu, Masayuki
;           Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
;     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;     STREET: 268 BUSH STREET, SUITE 3200
;     CITY: SAN FRANCISCO
;     STATE: CALIFORNIA
;     COUNTRY: USA
;     ZIP: 94104
; COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/256,702
;     FILING DATE: 27-Sep-2002
;     CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/933,261
;     FILING DATE: 20-Aug-2001
;     APPLICATION NUMBER: 08/808,982
;     FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;     NAME: OSMAN, RICHARD A
;     REGISTRATION NUMBER: 36,627
;     REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (415) 343-4341
;     TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 5:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 898 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: No. US20030059859A1 Relevant
;         TOPOLOGY: No. US20030059859A1 Relevant
;     MOLECULE TYPE: peptide
;     SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-256-702-5

```

```

Query Match          100.0%;  Score 326;  DB 14;  Length 898;
Best Local Similarity 100.0%;  Pred. No. 1.1e-29;
Matches    61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy      1  EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      163 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 222

Qy      61  A  61
        |
Db      223  A  223

```

RESULT 6

US-10-240-154-16
; Sequence 16, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-240-154-16

Query Match 100.0%; Score 326; DB 14; Length 898;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
|
Db 163 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 222

Qy 61 A 61
|
Db 223 A 223

RESULT 7

US-10-624-932-2
; Sequence 2, Application US/10624932
; Publication No. US20040096877A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennnda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

```

; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-624-932-2

```

```

Query Match          100.0%; Score 326; DB 15; Length 898;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      163 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 222

Qy      61 A 61
          |
Db      223 A 223

```

```

RESULT 8
US-09-970-944-2
; Sequence 2, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138

```

; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 899
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-944-2

Query Match 100.0%; Score 326; DB 10; Length 899;
Best Local Similarity 100.0%; Pred. No. 1.1e-29;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPEGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCV 60
|
Db 163 EQGIVLPCRPEGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCV 222

Qy 61 A 61
|
Db 223 A 223

RESULT 9

US-09-970-944-15

; Sequence 15, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1e1 Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-970-944-15

Query Match 75.2%; Score 245; DB 10; Length 931;
Best Local Similarity 68.9%; Pred. No. 4.5e-20;
Matches 42; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPEGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCV 60
|| ::| ||||| |||||:|::|: | | ||| :|:|::| |||||
Db 181 EQEVLLQCRPEGIPVAEVEWLKNEIIDPAEDRNFYITIDHNLIKQARLSDTANYTCV 240

Qy 61 A 61
 |
Db 241 A 241

RESULT 10

US-09-972-211-121

; Sequence 121, Application US/09972211
; Publication No. US20040048245A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennda
; APPLICANT: Szekeres Jr, Edward S
; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides
Encoding Them And
; TITLE OF INVENTION: Methods Of Using The Same
; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06

```
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
;   LENGTH: 931
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-972-211-121
```

```
Query Match          75.2%; Score 245; DB 11; Length 931;
Best Local Similarity 68.9%; Pred. No. 4.5e-20;
Matches    42; Conservative    12; Mismatches    7; Indels    0; Gaps    0;
```

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Qy      1 EQGIVLPCRPEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCV 60
      || ::| ||||| |||||:|:|:|:| | | ||| :|:|:|:|:|:|:|:|:|
Db     181 EQEVLLQCRPPEGIPVAEVEWLKNEDIIDPAEDRNFYITIDHNLIIKQARLSDTANYTCV 240

Qy      61 A 61
      |
Db     241 A 241
```

RESULT 11

US-10-087-684-35

```
; Sequence 35, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Cathereine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
```

```
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 35
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-684-35
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```
Query Match          75.2%; Score 245; DB 15; Length 931;
Best Local Similarity 68.9%; Pred. No. 4.5e-20;
Matches 42; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
      || ::| ||||| |||||:||||:| | ||| :|:|::| |||:|||||
Db      181 EQEVLQCRPPEGIPVAEVEWLKNEDIIDPAEDRNFYITIDHNLIKQARLSDTANYTCV 240

Qy      61 A 61
      |
Db      241 A 241
```

RESULT 12

```
US-10-037-417-117
; Sequence 117, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
```



```

; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-037-417-117

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Query Match          75.2%; Score 245; DB 15; Length 931;
Best Local Similarity 68.9%; Pred. No. 4.5e-20;
Matches 42; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

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Qy      1 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
        || :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 EQEVLQCRPPGIPVAEVEWLKNEIDIIDPAEDRNFYITIDHNLIIKQARLSDTANYTCV 240

Qy      61 A 61
        |
Db      241 A 241

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RESULT 13
US-10-096-625-121

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; Sequence 121, Application US/10096625
; Publication No. US20040068095A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennnda
; APPLICANT: Szekeres Jr, Edward S
; APPLICANT: Ji, Weizhen
; TITLE OF INVENTION: No. US20040068095A1el Human Proteins, Polynucleotides
Encoding Them And
; TITLE OF INVENTION: Methods Of Using The Same
; FILE REFERENCE: 21402-141 CIP
; CURRENT APPLICATION NUMBER: US/10/096,625
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/972,211
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: 60/275,892
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/296,860
 ; PRIOR FILING DATE: 2001-06-08
 ; NUMBER OF SEQ ID NOS: 200
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 121
 ; LENGTH: 931
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-096-625-121

Query Match 75.2%; Score 245; DB 15; Length 931;
 Best Local Similarity 68.9%; Pred. No. 4.5e-20;
 Matches 42; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPEGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCV 60
 || ::| ||||| |||||:|:|:| | | || |:|:|:|:|:|:|:|
 Db 181 EQEVLLQCRPPEGIPVAEVEWLKNEDIIDPAEDRNFYITIDHNLIKQARLSDTANYTCV 240
 Qy 61 A 61
 |
 Db 241 A 241

RESULT 14

US-10-218-779-35

; Sequence 35, Application US/10218779

; Publication No. US20040029222A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit
 ; APPLICANT: MacDougall, John
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Stone, David
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Grosse, William
 ; APPLICANT: Alsobrook II, John
 ; APPLICANT: Lepley, Denise
 ; APPLICANT: Rieger, Daniel
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Casman, Stacie
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Boldog, Ferenc
 ; APPLICANT: Li, Li
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Mishra, Vishnu
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Gangolli, Esha

```
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-218-779-35
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```
Query Match          75.2%; Score 245; DB 15; Length 1010;
Best Local Similarity 68.9%; Pred. No. 5e-20;
Matches 42; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
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Qy      1 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCV 60
      || ::| ||||| |||||:|:|:|:| | | || |:|:|:|:|:|:|:|:|:|:|
Db      181 EQEVLLQCRPPGIPVAEVEWLKNEDIIDPAEDRNFYITIDHNLIIKQARLSDTANYTCV 240

Qy      61 A 61
      |
Db      241 A 241
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RESULT 15

```
US-09-970-944-16
; Sequence 16, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1 Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
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US-09-970-944-16

Query Match 74.2%; Score 242; DB 10; Length 931;
Best Local Similarity 68.9%; Pred. No. 1e-19;
Matches 42; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

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Qy      1 EQGIVLPCRPEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCV 60
          || ::| ||||| |||||:||||:| | ||| :|:|::| |||:|||||
Db     181 EQEVLLQCRPPEGIPVAEVEWLKNEDIIDPVEDRNFYITIDHNLIKQARLSDTANYTCV 240

Qy      61 A 61
          |
Db     241 A 241
```

Search completed: March 1, 2005, 09:51:29
Job time : 11.7404 secs

OM protein - protein search, using sw model

Run on: March 1, 2005, 08:41:47 ; Search time 11.1589 Seconds
 (without alignments)
 2799.282 Million cell updates/sec

Title: US-10-624-932-2_COPY_163_223
 Perfect score: 326
 Sequence: 1 EQGIVLPCRPPGEGIPPAEVE.....HSLVVRQARLADTANYTCVA 61

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	326	100.0	842	1	UN5A_HUMAN	Q6zn44 homo sapien
2	326	100.0	898	1	UN5A_MOUSE	Q8kls4 mus musculu
3	326	100.0	898	1	UN5A_RAT	O08721 rattus norv
4	245	75.2	931	1	UN5C_MOUSE	O08747 mus musculu
5	242	74.2	931	1	UN5C_HUMAN	O95185 homo sapien
6	242	74.2	931	1	UN5C_RAT	Q761x5 rattus norv
7	237	72.7	931	1	UN5C_CHICK	Q7t2z5 gallus gall
8	236	72.4	943	1	UN5B_XENLA	Q8jgt4 xenopus lae
9	230	70.6	945	1	UN5B_HUMAN	Q8izj1 homo sapien
10	230	70.6	945	1	UN5B_MOUSE	Q8kls3 mus musculu
11	230	70.6	945	1	UN5B_RAT	O08722 rattus norv
12	217	66.6	199	1	UNC5_PETMA	Q9pvd5 petromyzon
13	201	61.7	953	1	UN5D_HUMAN	Q6uxz4 homo sapien
14	201	61.7	956	1	UN5D_MOUSE	Q8kls2 mus musculu
15	123	37.7	919	1	UNC5_CAEEL	Q26261 caenorhabdi

16	105	32.2	1224	2	O00533	O00533 homo sapien
17	104	31.9	759	2	Q7PW77	Q7pw77 anopheles g
18	103	31.6	424	2	Q8C6W0	Q8c6w0 mus musculu
19	103	31.6	1150	2	Q8BS24	Q8bs24 mus musculu
20	103	31.6	1209	2	P70232	P70232 mus musculu
21	98	30.1	848	2	Q25198	Q25198 hydra atten
22	97	29.8	1450	1	MPSF_CHICK	Q02173 gallus gall
23	96	29.4	789	2	Q7PME2	Q7pme2 anopheles g
24	96	29.4	2673	2	Q96SC3	Q96sc3 homo sapien
25	96	29.4	5636	2	Q96RW7	Q96rw7 homo sapien
26	95.5	29.3	1072	1	UNC5_DROME	Q95tu8 drosophila
27	95	29.1	1154	2	Q9QVN3	Q9qvn3 rattus sp.
28	95	29.1	1194	2	Q6PW35	Q6pw35 rattus norv
29	95	29.1	1197	2	Q6PW38	Q6pw38 rattus norv
30	95	29.1	1198	2	Q6PW37	Q6pw37 rattus norv
31	95	29.1	1206	2	Q6PW36	Q6pw36 rattus norv
32	95	29.1	1209	2	Q6PW39	Q6pw39 rattus norv
33	95	29.1	1214	1	NRCA_RAT	P97686 rattus norv
34	95	29.1	1256	1	NRCA_MOUSE	Q810u4 mus musculu
35	95	29.1	1299	2	Q6PW34	Q6pw34 rattus norv
36	94	28.8	1266	1	NGCA_CHICK	Q03696 gallus gall
37	94	28.8	1280	2	Q90933	Q90933 gallus gall
38	92.5	28.4	865	2	Q68DA2	Q68da2 homo sapien
39	92.5	28.4	1040	1	AXO1_HUMAN	Q02246 homo sapien
40	92.5	28.4	1040	1	AXO1_MOUSE	Q61330 mus musculu
41	92.5	28.4	1040	1	AXO1_RAT	P22063 rattus norv
42	92	28.2	1166	2	Q9QVN4	Q9qvn4 rattus sp.
43	91.5	28.1	926	2	Q7LDM3	Q7ldm3 homo sapien
44	91.5	28.1	1019	2	Q9Y6L9	Q9y6l9 homo sapien
45	91.5	28.1	2154	2	Q8WZ51	Q8wz51 homo sapien

ALIGNMENTS

RESULT 1

UN5A_HUMAN

ID UN5A_HUMAN STANDARD; PRT; 842 AA.

AC Q6ZN44; Q8TF26; Q96GP4;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).

GN Name=UNC5A; Synonyms=KIAA1976, UNC5H1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX PubMed=14702039; DOI=10.1038/ng1285;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,

RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 302-842 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 624-728 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21842142; PubMed=11853319;
 RA Nagase T., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XXII.
 RT The complete sequences of 50 new cDNA clones which code for large

RT proteins.";

RL DNA Res. 8:319-327(2001).

RN [4]

RP INDUCTION.

RX PubMed=12598906; DOI=10.1038/ncb943;

RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;

RT "p53RDL1 regulates of p53-dependent apoptosis.";

RL Nat. Cell Biol. 5:216-223(2003).

RN [5]

RP DOWN-REGULATION IN CANCER.

RX PubMed=12655055; DOI=10.1073/pnas.0738063100;

RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,

RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;

RT "The netrin-1 receptors UNC5H are putative tumor suppressors

RT controlling cell death commitment.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).

CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates

CC axon repulsion of neuronal growth cones in the developing nervous

CC system upon ligand binding. Axon repulsion in growth cones may be

CC caused by its association with DCC that may trigger signaling for

CC repulsion. It also acts as a dependence receptor required for

CC apoptosis induction when not associated with netrin ligand.

CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts

CC with MAGED1. Interacts with PRKCABP, possibly mediating some

CC interaction with PKC (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction

CC with PRKCABP regulates its surface expression and leads to its

CC removal from surface of neurons and growth cones (By similarity).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Name=1;

CC IsoId=Q6ZN44-1; Sequence=Displayed;

CC Note=No experimental confirmation available;

CC Name=2;

CC IsoId=Q6ZN44-2; Sequence=VSP_011694, VSP_011695;

CC Note=No experimental confirmation available;

CC Name=3;

CC IsoId=Q6ZN44-3; Sequence=VSP_011693;

CC Note=No experimental confirmation available;

CC -!- INDUCTION: By p53/TP53.

CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which

CC participates in the induction of apoptosis (By similarity).

CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues.

CC Phosphorylated by PKC in vitro (By similarity).

CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The

CC cleavage does not take place when the receptor is associated with

CC netrin ligand. Its cleavage by caspases is required to induce

CC apoptosis (By similarity).

CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including

CC colorectal, breast, ovary, uterus, stomach, lung, or kidney

CC cancers.

CC -!- SIMILARITY: Belongs to the UNC-5 family.

CC -!- SIMILARITY: Contains 1 death domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC -!- SIMILARITY: Contains 1 TSP type-1 domain.

CC -!- SIMILARITY: Contains 1 ZU5 domain.

SQ SEQUENCE 842 AA; 92958 MW; 3DFADCF973131849 CRC64;

Query Match 100.0%; Score 326; DB 1; Length 842;
Best Local Similarity 100.0%; Pred. No. 2e-30;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
|
Db 163 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 222

Qy 61 A 61
|
Db 223 A 223

RESULT 2

UN5A_MOUSE

ID UN5A_MOUSE STANDARD; PRT; 898 AA.
AC Q8K1S4; Q6PEF7; Q80T71;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
GN Name=Unc5a; Synonyms=Kiaa1976, Unc5h1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
RA Engelkamp D.;
RT "Cloning of three mouse unc-5 genes and their expression patterns at
RT mid-gestation.";
RL Mech. Dev. 118:191-197(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:35-48(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand (By
 CC similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with MAGED1. Interacts with PRKCABP, possibly mediating some
 CC interaction with PKC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
 CC with PRKCABP regulates its surface expression and leads to its
 CC removal from surface of neurons and growth cones (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q8K1S4-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8K1S4-2; Sequence=VSP_011697;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=Q8K1S4-3; Sequence=VSP_011696;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Restricted to central nervous system.
 CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
 CC participates in the induction of apoptosis (By similarity).
 CC -!- PTM: Phosphorylated by PKC in vitro. Phosphorylated on cytoplasmic
 CC tyrosine residues (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----

DR EMBL; AJ487852; CAD32250.1; -.
 DR EMBL; AK122575; BAC65857.1; ALT_INIT.
 DR EMBL; BC058084; AAH58084.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:894682; Unc5a.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.

KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.

FT	SIGNAL	1	25	Potential.
FT	CHAIN	26	898	Netrin receptor UNC5A.
FT	DOMAIN	26	361	Extracellular (Potential).
FT	TRANSMEM	362	382	Potential.
FT	DOMAIN	383	898	Cytoplasmic (Potential).
FT	DOMAIN	44	141	Ig-like.
FT	DOMAIN	155	234	Ig-like C2-type.
FT	DOMAIN	242	296	TSP type-1 1.
FT	DOMAIN	298	350	TSP type-1 2.
FT	DOMAIN	495	598	ZU5.
FT	DOMAIN	817	897	Death.
FT	SITE	396	397	Cleavage (by caspase-3) (By similarity).
FT	SITE	661	679	Interaction with DCC (By similarity).
FT	DISULFID	65	124	By similarity.
FT	DISULFID	170	221	By similarity.
FT	CARBOHYD	107	107	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	218	218	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	343	343	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	1	790	Missing (in isoform 3).
FT				/FTId=VSP_011696.
FT	VARSPLIC	241	296	Missing (in isoform 2).
FT				/FTId=VSP_011697.
FT	CONFLICT	217	217	A -> P (in Ref. 3).
SQ	SEQUENCE	898 AA;	98856 MW;	59F04BA2E196C1DB CRC64;

Query Match 100.0%; Score 326; DB 1; Length 898;
 Best Local Similarity 100.0%; Pred. No. 2.2e-30;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDP SLDPNVYITREHSLVVRQARLADTANYTCV 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     163 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDP SLDPNVYITREHSLVVRQARLADTANYTCV 222

Qy      61 A 61
          |
Db     223 A 223
```

RESULT 3

UN5A_RAT

ID UN5A_RAT STANDARD; PRT; 898 AA.
AC 008721;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
GN Name=Unc5a; Synonyms=Unc5h1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Ventral spinal cord;
RX MEDLINE=97271897; PubMed=9126742;
RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,
RA Tessier-Lavigne M.;
RT "Vertebrate homologues of C. elegans UNC-5 are candidate netrin
RT receptors.";
RL Nature 386:833-838(1997).
RN [2]
RP FUNCTION, AND INTERACTION WITH DCC.
RX PubMed=10399920;
RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
RA Stein E.;
RT "A ligand-gated association between cytoplasmic domains of UNC5 and
RT DCC family receptors converts netrin-induced growth cone attraction to
RT repulsion.";
RL Cell 97:927-941(1999).
RN [3]
RP TISSUE SPECIFICITY.
RX PubMed=11472849;
RA Barrett C., Guthrie S.;
RT "Expression patterns of the netrin receptor UNC5H1 among developing
RT motor neurons in the embryonic rat hindbrain.";
RL Mech. Dev. 106:163-166(2001).
RN [4]
RP FUNCTION.
RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
RL EMBO J. 20:2715-2722(2001).
RN [5]

RP FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION WITH MAGED1.
 RX PubMed=12598531; DOI=10.1074/jbc.M300415200;
 RA Williams M.E., Strickland P., Watanabe K., Hinck L.;
 RT "UNC5H1 induces apoptosis via its juxtamembrane region through an
 RT interaction with NRAGE.";
 RL J. Biol. Chem. 278:17483-17490(2003).
 RN [6]
 RP INTERACTION WITH PRKCABP, PHOSPHORYLATION, AND MUTAGENESIS OF
 RP 896-ALA--CYS-898.
 RX PubMed=14672991; DOI=23/36/11279;
 RA Williams M.E., Wu S.C.-Y., McKenna W.L., Hinck L.;
 RT "Surface expression of the netrin receptor UNC5H1 is regulated through
 RT a protein kinase C-interacting protein/protein kinase-dependent
 RT mechanism.";
 RL J. Neurosci. 23:11279-11288(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with MAGED1. Interacts with PRKCABP, possibly mediating some
 CC interaction with PKC.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
 CC with PRKCABP regulates its surface expression and leads to its
 CC removal from surface of neurons and growth cones.
 CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
 CC neurons. Expressed at early stages of neural tube development in
 CC the ventral spinal cord. In developing hindbrain, it colocalizes
 CC with a number of cranial motor neuron subpopulations from
 CC embryonic E11 to E14, while DCC is expressed by motor neurons at
 CC E12. Also expressed in non-neural structures, such as the basal
 CC plane of the hindbrain and midbrain, in the developing
 CC hypothalamus, thalamus and in the pallidum.
 CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
 CC participates in the induction of apoptosis.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity). Phosphorylated by PKC in vitro.
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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CC -----
DR EMBL; U87305; AAB57678.1; -.
DR HSSP; P07996; 1LSL.
DR RGD; 621755; Unc5h1.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Apoptosis; Developmental protein; Immunoglobulin domain;
KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 898 Netrin receptor UNC5A.←
FT DOMAIN 26 361 Extracellular (Potential).
FT TRANSMEM 362 382 Potential.
FT DOMAIN 383 898 Cytoplasmic (Potential).
FT DOMAIN 44 141 Ig-like.
FT DOMAIN 155 238 Ig-like C2-type.
FT DOMAIN 242 296 TSP type-1 1.←
FT DOMAIN 298 350 TSP type-1 2.←
FT DOMAIN 495 598 ZU5.←
FT DOMAIN 817 897 Death.←
FT SITE 396 397 Cleavage (by caspase-3) (By similarity).
FT SITE 661 679 Interaction with DCC (By similarity).
FT DISULFID 65 124 By similarity.
FT DISULFID 170 221 By similarity.
FT CARBOHYD 107 107 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 218 218 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 343 343 N-linked (GlcNAc . . .) (Potential).
FT MUTAGEN 896 898 Missing: Abolishes interaction with
FT PRKCABP.
SQ SEQUENCE 898 AA; 98840 MW; 7A3CBCB9E7ACA135 CRC64;

```

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Query Match 100.0%; Score 326; DB 1; Length 898;
Best Local Similarity 100.0%; Pred. No. 2.2e-30;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 163 EQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV 222

Qy 61 A 61
   |

```


RESULT 4

UN5C_MOUSE

ID UN5C_MOUSE STANDARD; PRT; 931 AA.
AC O08747; Q8CD16;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)
DE (Rostral cerebellar malformation protein).
GN Name=Unc5c; Synonyms=Rcm, Unc5h3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, DISEASE, AND TISSUE
RP SPECIFICITY.
RC STRAIN=C57B6/SJL;
RX MEDLINE=97271898; PubMed=9126743;
RA Ackerman S.L., Kozak L.P., Przyborski S.A., Rund L.A., Boyer B.B.,
RA Knowles B.B.;
RT "The mouse rostral cerebellar malformation gene encodes an UNC-5-like
RT protein.";
RL Nature 386:838-842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [3]

RP FUNCTION, AND TISSUE SPECIFICITY.

RX PubMed=9389662;

RA Przyborski S.A., Knowles B.B., Ackerman S.L.;

RT "Embryonic phenotype of Unc5h3 mutant mice suggests chemorepulsion
 RT during the formation of the rostral cerebellar boundary.";

RL Development 125:41-50(1998).

RN [4]

RP INTERACTION WITH DCC.

RX PubMed=10399920;

RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
 RA Stein E.;

RT "A ligand-gated association between cytoplasmic domains of UNC5 and
 RT DCC family receptors converts netrin-induced growth cone attraction to
 RT repulsion.";

RL Cell 97:927-941(1999).

RN [5]

RP PHOSPHORYLATION SITE TYR-568, AND MUTAGENESIS OF TYR-568.

RX PubMed=11533026; DOI=10.1074/jbc.M103872200;

RA Tong J., Killeen M., Steven R., Binns K.L., Culotti J., Pawson T.;

RT "Netrin stimulates tyrosine phosphorylation of the UNC-5 family of
 RT netrin receptors and induces Shp2 binding to the RCM cytodomain.";

RL J. Biol. Chem. 276:40917-40925(2001).

RN [6]

RP FUNCTION.

RX PubMed=12451134; DOI=22/23/10346;

RA Finger J.H., Bronson R.T., Harris B., Johnson K., Przyborski S.A.,
 RA Ackerman S.L.;

RT "The netrin 1 receptors Unc5h3 and Dcc are necessary at multiple
 RT choice points for the guidance of corticospinal tract axons.";

RL J. Neurosci. 22:10346-10356(2002).

CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. Also involved in corticospinal tract axon guidances
 CC independently of DCC. It also acts as a dependence receptor
 CC required for apoptosis induction when not associated with netrin
 CC ligand.

CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=008747-1; Sequence=Displayed;

CC Name=2;

CC IsoId=008747-2; Sequence=VSP_011702;

CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
 CC neurons. Highly expressed in brain and lung. Weakly expressed in
 CC testis, ovary, spleen, thymus and bladder. Expressed at very low
 CC level in kidney, intestine and salivary gland.

CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
 CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
 CC phosphatase, suggesting that its activity is regulated by

CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
 CC netrin-dependent.
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- DISEASE: Defects in Unc5c are the cause of rostral cerebellar
 CC malformation (Rcm). Rcm is characterized by cerebellar and
 CC midbrain defects, apparently as a result of abnormal neuronal
 CC migration.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; U72634; AAB54103.1; -.
 DR EMBL; AK031655; BAC27495.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:1095412; Unc5c.
 DR GO; GO:0005886; C:plasma membrane; IC.
 DR GO; GO:0005042; F:netrin receptor activity; IDA.
 DR GO; GO:0005515; F:protein binding; IDA.
 DR GO; GO:0007420; P:brain development; IMP.
 DR GO; GO:0030334; P:regulation of cell migration; IMP.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 40 Potential.

FT	CHAIN	41	931	Netrin receptor UNC5C.
FT	DOMAIN	41	380	Extracellular (Potential).
FT	TRANSMEM	381	401	Potential.
FT	DOMAIN	402	931	Cytoplasmic (Potential).
FT	DOMAIN	62	159	Ig-like.
FT	DOMAIN	161	256	Ig-like C2-type.
FT	DOMAIN	260	314	TSP type-1 1.
FT	DOMAIN	316	368	TSP type-1 2.
FT	DOMAIN	528	631	ZU5.
FT	DOMAIN	850	929	Death.
FT	SITE	415	416	Cleavage (by caspase-3) (By similarity).
FT	SITE	694	712	Interaction with DCC (By similarity).
FT	DISULFID	83	142	By similarity.
FT	DISULFID	188	239	By similarity.
FT	MOD_RES	568	568	Phosphotyrosine.
FT	CARBOHYD	236	236	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	361	361	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	370	370	A -> GFYPISTEHRPQNEYGFSS (in isoform 2).
FT				/FTId=VSP_011702.
FT	MUTAGEN	568	568	Y->F: Abolishes interaction with PTPN11,
FT				leading to a increased level of
FT				phosphorylation.
FT	CONFLICT	16	16	L -> I (in Ref. 2).
FT	CONFLICT	733	733	H -> R (in Ref. 2).
FT	CONFLICT	924	924	S -> Y (in Ref. 2).
SQ	SEQUENCE	931 AA;	103062 MW;	8A5D951A4EECA179 CRC64;

Query Match 75.2%; Score 245; DB 1; Length 931;
 Best Local Similarity 68.9%; Pred. No. 1.4e-20;
 Matches 42; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy	1	EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCV	60
		:: : :: : : : :: : : :	
Db	181	EQEVLLQCRPPGEGIPVAEVEWLKNEDIIDPAEDRNFYITIDHNLIIKQARLSDTANYTCV	240
Qy	61	A 61	
Db	241	A 241	

RESULT 5

UNC5_HUMAN

ID UNC5_HUMAN STANDARD; PRT; 931 AA.
 AC O95185; Q8IUT0;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3).
 GN Name=UNC5C; Synonyms=UNC5H3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
 RC TISSUE=Brain;
 RX MEDLINE=99000841; PubMed=9782087; DOI=10.1006/geno.1998.5425;

RA Ackerman S.L., Knowles B.B.;
 RT "Cloning and mapping of the UNC5C gene to human chromosome 4q21-q23.";
 RL Genomics 52:205-208(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP DOWN-REGULATION IN CANCER.
 RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
 RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
 RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
 RT "The netrin-1 receptors UNC5H are putative tumor suppressors
 RT controlling cell death commitment.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. Also involved in corticospinal tract axon guidances
 CC independently of DCC. It also acts as a dependence receptor
 CC required for apoptosis induction when not associated with netrin
 CC ligand (By similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O95185-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O95185-2; Sequence=VSP_011700, VSP_011701;
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in
 CC kidney. Not expressed in developing or adult lung.
 CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
 CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
 CC phosphatase, suggesting that its activity is regulated by

CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
 CC netrin-dependent (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
 CC colorectal, breast, ovary, uterus, stomach, lung, or kidney
 CC cancers.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF055634; AAC67491.1; -.
 DR EMBL; BC041156; AAH41156.1; -.
 DR HSSP; P07996; 1LSL.
 DR Genew; HGNC:12569; UNC5C.
 DR MIM; 603610; -.
 DR GO; GO:0005042; F:netrin receptor activity; TAS.
 DR GO; GO:0007411; P:axon guidance; TAS.
 DR GO; GO:0007420; P:brain development; TAS.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Polymorphism; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 40 Potential.
 FT CHAIN 41 931 Netrin receptor UNC5C.
 FT DOMAIN 41 380 Extracellular (Potential).

FT	TRANSMEM	381	401	Potential.
FT	DOMAIN	402	931	Cytoplasmic (Potential).
FT	DOMAIN	62	159	Ig-like.
FT	DOMAIN	161	256	Ig-like C2-type.
FT	DOMAIN	260	314	TSP type-1 1.
FT	DOMAIN	316	368	TSP type-1 2.
FT	DOMAIN	528	631	ZU5.
FT	DOMAIN	850	929	Death.
FT	SITE	415	416	Cleavage (by caspase-3) (By similarity).
FT	SITE	694	712	Interaction with DCC (By similarity).
FT	DISULFID	83	142	By similarity.
FT	DISULFID	188	239	By similarity.
FT	MOD_RES	568	568	Phosphotyrosine (By similarity).
FT	CARBOHYD	236	236	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	361	361	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	370	370	T -> SFIYPISTEQRTQNEYGFSS (in isoform 2).
FT				/FTId=VSP_011700.
FT	VARSPLIC	579	931	Missing (in isoform 2).
FT				/FTId=VSP_011701.
FT	VARIANT	37	37	G -> V (in dbSNP:2306715).
FT				/FTId=VAR_019731.
FT	VARIANT	721	721	T -> M (in dbSNP:2289043).
FT				/FTId=VAR_019732.
FT	CONFLICT	219	219	T -> I (in Ref. 1).
FT	CONFLICT	489	489	S -> T (in Ref. 1).
SQ	SEQUENCE	931 AA;	103101 MW;	EFD71122C98DABB8 CRC64;

Query Match 74.2%; Score 242; DB 1; Length 931;
 Best Local Similarity 68.9%; Pred. No. 3.2e-20;
 Matches 42; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy	1	EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCV	60
		: : : : : : : : : : : : :	
Db	181	EQEVLLQCRPPGEGIPVAEVEWLKNEDIIDPVEDRNFYITIDHNLIIKQARLSDTANYTCV	240
Qy	61	A 61	
Db	241	A 241	

RESULT 6

UN5C_RAT

ID UN5C_RAT STANDARD; PRT; 931 AA.
 AC Q761X5;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3).
 GN Name=Unc5c; Synonyms=Unc5h3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND DISEASE.
 RX PubMed=15010202; DOI=10.1016/j.molbrainres.2003.12.003;
 RA Kuramoto T., Kuwamura M., Serikawa T.;

RT "Rat neurological mutations cerebellar vermis defect and hobble are
RT caused by mutations in the netrin-1 receptor gene Unc5h3.";
RL Brain Res. Mol. Brain Res. 122:103-108(2004).
RN [2]
RP FUNCTION.
RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
RL EMBO J. 20:2715-2722(2001).

CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. Also involved in corticospinal tract axon guidances
CC independently of DCC. It also acts as a dependence receptor
CC required for apoptosis induction when not associated with netrin
CC ligand.

CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
CC similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in
CC kidney. Not expressed in developing or adult lung.

CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
CC phosphatase, suggesting that its activity is regulated by
CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
CC netrin-dependent (By similarity).

CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis.

CC -!- DISEASE: Defects in Unc5c are the cause of cerebellar vermis
CC defect (cvd) and hobble (hob) phenotypes. Cvd and hob rats exhibit
CC cerebellar and midbrain defects, possibly as a result of abnormal
CC neuronal migration, and exhibit laminar structure abnormalities in
CC the fused cerebellar hemispheres and ectopic cerebellar tissues in
CC the cerebello-pontine junction.

CC -!- SIMILARITY: Belongs to the UNC-5 family.

CC -!- SIMILARITY: Contains 1 death domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC -!- SIMILARITY: Contains 2 TSP type-1 domains.

CC -!- SIMILARITY: Contains 1 ZU5 domain.

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CC -----

DR EMBL; AB118026; BAD05181.1; -.

DR RGD; 735109; Unc5c.

DR InterPro; IPR000488; Death.

DR InterPro; IPR011029; DEATH_like.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 40 Potential.
 FT CHAIN 41 931 Netrin receptor UNC5C.
 FT DOMAIN 41 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 931 Cytoplasmic (Potential).
 FT DOMAIN 62 159 Ig-like.
 FT DOMAIN 161 256 Ig-like C2-type.
 FT DOMAIN 260 314 TSP type-1 1.
 FT DOMAIN 316 368 TSP type-1 2.
 FT DOMAIN 528 631 ZU5.
 FT DOMAIN 850 929 Death.
 FT SITE 415 416 Cleavage (by caspase-3) (By similarity).
 FT SITE 694 712 Interaction with DCC (By similarity).
 FT DISULFID 83 142 By similarity.
 FT DISULFID 188 239 By similarity.
 FT MOD_RES 568 568 Phosphotyrosine (By similarity).
 FT CARBOHYD 236 236 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 361 361 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 931 AA; 103134 MW; 25B183A97BCB8401 CRC64;

Query Match 74.2%; Score 242; DB 1; Length 931;
 Best Local Similarity 68.9%; Pred. No. 3.2e-20;
 Matches 42; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCV 60
 || ::| ||||| |||||:|::|| | | ||| :|:|::| |||:| |||||
 Db 181 EQEVLLQCRPPEGIPMAEVEWLKNEDIIDPVEDRNFYITIDHNLIIKQARLSDTANYTCV 240
 QY 61 A 61
 |
 Db 241 A 241

RESULT 7
 UN5C_CHICK
 ID UN5C_CHICK STANDARD; PRT; 931 AA.
 AC Q7T2Z5;

DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)
 DE (cUNC-5H3).
 GN Name=UNC5C;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX PubMed=12799087;
 RA Guan W., Condic M.L.;
 RT "Characterization of Netrin-1, Neogenin and cUNC-5H3 expression during
 RT chick dorsal root ganglia development.";
 RL Gene Expr. Patterns 3:369-373(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Restricted to proprioceptive neurons.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AY187310; AAO67275.1; -.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.

KW	Developmental protein; Immunoglobulin domain; Phosphorylation;			
KW	Receptor; Repeat; Signal; Transmembrane.			
FT	SIGNAL	1	39	Potential.
FT	CHAIN	40	931	Netrin receptor UNC5C.
FT	DOMAIN	40	380	Extracellular (Potential).
FT	TRANSMEM	381	401	Potential.
FT	DOMAIN	402	931	Cytoplasmic (Potential).
FT	DOMAIN	62	159	Ig-like.
FT	DOMAIN	161	256	Ig-like C2-type.
FT	DOMAIN	260	314	TSP type-1 1.
FT	DOMAIN	316	368	TSP type-1 2.
FT	DOMAIN	528	631	ZU5.
FT	DOMAIN	850	929	Death.
FT	DISULFID	83	142	By similarity.
FT	DISULFID	188	239	By similarity.
FT	CARBOHYD	236	236	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	361	361	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE 931 AA; 102906 MW; 1E23A0D84F2E2C62 CRC64;			

```

Qy      1 EQGIVLPCRPPGEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCV 60
      || ::| ||||| |||||:|:::| | | | | :|:|::| |||:|||||
Db     181 EQEVLLQCRPPEGIPVAEVEWLKNEEVIDPVEDRNFYITIDHNLIQKARLSDTANYTCV 240

Qy      61 A 61
      |
Db     241 A 241

```

CC restricted to the dorsal ciliary marginal zone, a site of
 CC retinoblast proliferation and differentiation.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AY099459; AAM34486.1; -.
 DR HSSP; P07996; 1LSL.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Developmental protein; Immunoglobulin domain; Phosphorylation;
 KW Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 30 Potential.
 FT CHAIN 31 943 Netrin receptor UNC5B.
 FT DOMAIN 31 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 943 Cytoplasmic (Potential).
 FT DOMAIN 51 148 Ig-like.
 FT DOMAIN 150 245 Ig-like C2-type.
 FT DOMAIN 249 303 TSP type-1 1.
 FT DOMAIN 305 357 TSP type-1 2.
 FT DOMAIN 540 643 ZU5.
 FT DOMAIN 863 941 Death.
 FT DISULFID 72 131 By similarity.
 FT DISULFID 177 228 By similarity.
 FT CARBOHYD 225 225 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 350 350 N-linked (GlcNAc. . .) (Potential).

SQ SEQUENCE 943 AA; 105083 MW; A024E24A7EDB6175 CRC64;

Query Match 72.4%; Score 236; DB 1; Length 943;
Best Local Similarity 63.9%; Pred. No. 1.7e-19;
Matches 39; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EQGIVLPCRPEGIPPAEVEWLRNEDLVDPSLDPNVYITREHSLVVRQARLADTANYTCV 60
|| :| |||||:|||||||:|::|: | | || :|:|::| |||:|||||||
Db 170 EQEALLQCRPPEGVPPAEVEWLKNEEIIDPTKDTNFLTIDHNLIIKQARLSDTANYTCV 229

Qy 61 A 61
:
Db 230 S 230

.RESULT 9

UN5B_HUMAN

ID UN5B_HUMAN STANDARD; PRT; 945 AA.
AC Q8IZJ1; Q86SN3; Q8N1Y2; Q9H9F3;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2)
DE (p53-regulated receptor for death and life protein 1)
DE (UNQ1883/PRO4326).
GN Name=UNC5B; Synonyms=P53RDL1, UNC5H2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION
RP WITH GNAI2.
RC TISSUE=Lung;
RX MEDLINE=22246081; PubMed=12359238; DOI=10.1016/S0006-291X(02)02277-5;
RA Komatsuzaki K., Dalvin S., Kinane T.B.;
RT "Modulation of G(ialpha(2)) signaling by the axonal guidance molecule
RT UNC5H2.";
RL Biochem. Biophys. Res. Commun. 297:898-905(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND MUTAGENESIS OF ASP-412.
RX PubMed=12598906; DOI=10.1038/ncb943;
RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;
RT "p53RDL1 regulates of p53-dependent apoptosis.";
RL Nat. Cell Biol. 5:216-223(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;

RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE OF 361-945 FROM N.A.
RC TISSUE=Amygdala, and Teratocarcinoma;
RX PubMed=14702039; DOI=10.1038/ngl285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiuji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [5]
RP DOWN-REGULATION IN CANCER.
RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
RT "The netrin-1 receptors UNC5H are putative tumor suppressors
RT controlling cell death commitment.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand.
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
CC similarity). Interacts with GNAI2 via its cytoplasmic part.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- ALTERNATIVE PRODUCTS:

```

CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=Q8IZJ1-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q8IZJ1-2; Sequence=VSP_011698;
CC      -!- TISSUE SPECIFICITY: Highly expressed in brain. Also expressed at
CC      lower level in developing lung, cartilage, kidney and
CC      hematopoietic and immune tissues.
CC      -!- INDUCTION: By p53/TP53.
CC      -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC      similarity).
CC      -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC      cleavage does not take place when the receptor is associated with
CC      netrin ligand. Its cleavage by caspases is required to induce
CC      apoptosis.
CC      -!- MISCELLANEOUS: Down-regulated in multiple cancers including
CC      colorectal, breast, ovary, uterus, stomach, lung, or kidney
CC      cancers.
CC      -!- SIMILARITY: Belongs to the UNC-5 family.
CC      -!- SIMILARITY: Contains 1 death domain.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC      -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC      -!- SIMILARITY: Contains 1 ZU5 domain.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AY126437; AAM95701.1; -.
DR      EMBL; AB096256; BAC57998.1; -.
DR      EMBL; AY358351; AAQ88717.1; -.
DR      EMBL; AK022859; BAB14276.1; ALT_INIT.
DR      EMBL; AK094595; BAC04382.1; ALT_INIT.
DR      HSSP; P07996; 1LSL.
DR      Genew; HGNC:12568; UNC5B.
DR      MIM; 607870; -.
DR      InterPro; IPR000488; Death.
DR      InterPro; IPR011029; DEATH_like.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003598; Ig_c2.
DR      InterPro; IPR000884; TSP1.
DR      InterPro; IPR008085; TSP_1.
DR      InterPro; IPR000906; ZU5.
DR      Pfam; PF00531; Death; 1.
DR      Pfam; PF00047; ig; 1.
DR      Pfam; PF00090; TSP_1; 2.
DR      Pfam; PF00791; ZU5; 1.
DR      PRINTS; PR01705; TSP1REPEAT.
DR      SMART; SM00005; DEATH; 1.
DR      SMART; SM00408; IGc2; 1.
DR      SMART; SM00209; TSP1; 2.
DR      SMART; SM00218; ZU5; 1.

```


RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
 RA Engelkamp D.;
 RT "Cloning of three mouse unc-5 genes and their expression patterns at
 RT mid-gestation.";
 RL Mech. Dev. 118:191-197(2002).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP TISSUE SPECIFICITY.
 RX PubMed=12799072;
 RA Dalvin S., Anselmo M.A., Prodhan P., Komatsuzaki K., Schnitzer J.J.,
 RA Kinane T.B.;
 RT "Expression of Netrin-1 and its two receptors DCC and UNC5H2 in the
 RT developing mouse lung.";
 RL Gene Expr. Patterns 3:279-283(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand (By
 CC similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with GNAI2 via its cytoplasmic part (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8K1S3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8K1S3-2; Sequence=VSP_011699;
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Expressed in lung
 CC during late development. Expressed during early blood vessel
 CC formation, in the semicircular canal and in a dorsal to ventral
 CC gradient in the retina.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AJ487853; CAD32251.1; -.
 DR EMBL; AK018177; BAB31108.1; -.
 DR EMBL; BC048162; AAH48162.1; ALT_INIT.

DR EMBL; BC057560; AAH57560.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:894703; Unc5b.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 945 Netrin receptor UNC5B.
 FT DOMAIN 27 377 Extracellular (Potential).
 FT TRANSMEM 378 398 Potential.
 FT DOMAIN 399 945 Cytoplasmic (Potential).
 FT DOMAIN 48 145 Ig-like.
 FT DOMAIN 153 242 Ig-like C2-type.
 FT DOMAIN 246 300 TSP type-1 1.
 FT DOMAIN 302 354 TSP type-1 2.
 FT DOMAIN 541 644 ZU5.
 FT DOMAIN 865 943 Death.
 FT SITE 412 413 Cleavage (by caspase-3) (By similarity).
 FT SITE 707 725 Interaction with DCC (By similarity).
 FT DISULFID 69 128 By similarity.
 FT DISULFID 174 225 By similarity.
 FT CARBOHYD 222 222 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 347 347 N-linked (GlcNAc . . .) (Potential).
 FT VARSPLIC 356 367 NQRTLNDPKSHP -> T (in isoform 2).
 FT /FTId=VSP_011699.
 FT CONFLICT 238 238 T -> A (in Ref. 2).
 FT CONFLICT 394 394 V -> E (in Ref. 2).
 FT CONFLICT 679 679 T -> S (in Ref. 2).
 FT CONFLICT 874 874 N -> D (in Ref. 2).
 SQ SEQUENCE 945 AA; 103738 MW; 80E896F0F0E06012 CRC64;

Query Match 70.6%; Score 230; DB 1; Length 945;
 Best Local Similarity 65.5%; Pred. No. 9.2e-19;
 Matches 38; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Qy 4 IVLPCRPPGEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVA 61
 ::| |||||:| |||||:||||:| | :| :|:|:|||||:|||||
 Db 170 VLLQCRPPEGVPVAEVEWLKNEVDIDPAQDTNFLTIDHNLIRQARLSDTANYTCVA 227

RESULT 11

UN5B_RAT

ID UN5B_RAT STANDARD; PRT; 945 AA.
AC 008722;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2).
GN Name=Unc5b; Synonyms=Unc5h2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RX MEDLINE=97271897; PubMed=9126742;
RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,
RA Tessier-Lavigne M.;
RT "Vertebrate homologues of C. elegans UNC-5 are candidate netrin
RT receptors.";
RL Nature 386:833-838(1997).
RN [2]
RP FUNCTION, AND INTERACTION WITH DCC.
RX PubMed=10399920;
RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
RA Stein E.;
RT "A ligand-gated association between cytoplasmic domains of UNC5 and
RT DCC family receptors converts netrin-induced growth cone attraction to
RT repulsion.";
RL Cell 97:927-941(1999).
RN [3]
RP FUNCTION, AND MUTAGENESIS OF ASP-412.
RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
RL EMBO J. 20:2715-2722(2001).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand.
CC -!- SUBUNIT: Interacts with GNAI2 via its cytoplasmic part (By
CC similarity). Interacts with the cytoplasmic part of DCC.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
CC neurons. Expressed in the developing sensory ganglia that flank
CC the spinal cord from E12, peaking at E14. Expressed in the roof
CC plate region of the spinal cord from E14.
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce

```

CC      apoptosis.
CC      -!- SIMILARITY: Belongs to the UNC-5 family.
CC      -!- SIMILARITY: Contains 1 death domain.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC      -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC      -!- SIMILARITY: Contains 1 ZU5 domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U87306; AAB57679.1; -.
DR      HSSP; P07996; 1LSL.
DR      RGD; 621756; Unc5h2.
DR      InterPro; IPR000488; Death.
DR      InterPro; IPR011029; DEATH_like.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003598; Ig_c2.
DR      InterPro; IPR000884; TSP1.
DR      InterPro; IPR008085; TSP_1.
DR      InterPro; IPR000906; ZU5.
DR      Pfam; PF00531; Death; 1.
DR      Pfam; PF00047; ig; 1.
DR      Pfam; PF00090; TSP_1; 2.
DR      Pfam; PF00791; ZU5; 1.
DR      PRINTS; PR01705; TSP1REPEAT.
DR      SMART; SM00005; DEATH; 1.
DR      SMART; SM00408; IGc2; 1.
DR      SMART; SM00209; TSP1; 2.
DR      SMART; SM00218; ZU5; 1.
DR      PROSITE; PS50017; DEATH_DOMAIN; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
DR      PROSITE; PS50092; TSP1; 2.
KW      Apoptosis; Developmental protein; Immunoglobulin domain;
KW      Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
FT      SIGNAL      1      26      Potential.
FT      CHAIN      27      945      Netrin receptor UNC5B.
FT      DOMAIN      27      377      Extracellular (Potential).
FT      TRANSMEM      378      398      Potential..
FT      DOMAIN      399      945      Cytoplasmic (Potential).
FT      DOMAIN      48      145      Ig-like.
FT      DOMAIN      153      242      Ig-like C2-type.
FT      DOMAIN      246      300      TSP type-1 1.
FT      DOMAIN      302      354      TSP type-1 2.
FT      DOMAIN      541      644      ZU5.
FT      DOMAIN      865      943      Death.
FT      SITE      412      413      Cleavage (by caspase-3).
FT      SITE      707      725      Interaction with DCC.
FT      DISULFID      69      128      By similarity.
FT      DISULFID      174      225      By similarity.
FT      CARBOHYD      222      222      N-linked (GlcNAc. . .) (Potential).
FT      CARBOHYD      347      347      N-linked (GlcNAc. . .) (Potential).

```

FT MUTAGEN 412 412 D->N: Abolishes cleavage by caspase-3 and
FT subsequent induction of apoptosis.
SQ SEQUENCE 945 AA; 103520 MW; 6E9C2A262E560B9B CRC64;

Query Match 70.6%; Score 230; DB 1; Length 945;
Best Local Similarity 65.5%; Pred. No. 9.2e-19;
Matches 38; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Qy 4 IVLPCRPPPEGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVA 61
::| |||||:| |||||:||||:| | :| :|:|:|||||:|||||||
Db 170 VLLQCRPPEGVPVAEVEWLKNEVDIDPAQDTNFLTIDHNLIRQARLSDTANYTCVA 227

RESULT 12

UNC5_PETMA

ID UNC5_PETMA STANDARD; PRT; 199 AA.
AC Q9PVD5;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor unc-5 homolog (Fragment).
GN Name=UNC-5;
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC TISSUE=Brain;
RX PubMed=11228949;
RA Shifman M.I., Selzer M.E.;
RT "Expression of the netrin receptor UNC-5 in lamprey brain: modulation
RT by spinal cord transection."
RL Neurorehabil. Neural Repair 14:49-58(2000).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in the spinal cord, primarily in
CC neurons of the lateral gray matter and in dorsal cells. Also
CC expressed in reticulospinal neurons.
CC -!- DEVELOPMENTAL STAGE: Following spinal cord transection, it is
CC strongly down-regulated at two weeks, during the period of axon
CC dieback. Up-regulated at three weeks, when many axons are
CC beginning to regenerate.
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC similarity).
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

```

CC -----
DR EMBL; AF129475; AAF00103.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Developmental protein; Immunoglobulin domain; Phosphorylation;
KW Receptor.
FT NON_TER      1      1
FT DOMAIN       <1    >199      Extracellular (Potential).
FT DOMAIN       103    192      Ig-like C2-type.
FT DISULFID     124    175      By similarity.
FT CARBOHYD     172    172      N-linked (GlcNAc. . .) (Potential).
FT NON_TER     199    199
SQ SEQUENCE    199 AA;  22911 MW;  C41F9CFC66D8DC0B CRC64;

```

```

Query Match          66.6%;  Score 217;  DB 1;  Length 199;
Best Local Similarity 60.3%;  Pred. No. 5.8e-18;
Matches   35;  Conservative   15;  Mismatches    8;  Indels    0;  Gaps    0;

```

```

Qy      4 IVLPCRPPGIPPAEVEWLRNEDLVDPVNYITREHSLVVRQARLADTANYTCVA 61
      ::| ||||: || |||||::|::|:| :| | ||| :|:|::| ||||:||||||
Db     120 VLLHCRPPDAIPQAEVEWLKSEEIIDPVIDQNFYITVDHNLIIKQTRLADSANYTCVA 177

```

RESULT 13

UN5D_HUMAN

```

ID UN5D_HUMAN STANDARD; PRT; 953 AA.
AC Q6UXZ4; Q8WYP7;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4)
DE (UNQ6012/PRO34692).
GN Name=UNC5D; Synonyms=KIAA1777, UNC5H4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [2]

```

RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RA Nakajima D., Nakayama M., Nagase T., Ohara O.;
 RT "Identification of unc5H4 gene.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Receptor for netrin. May be involved in axon guidance by
 CC mediating axon repulsion of neuronal growth cones in the
 CC developing nervous system upon ligand binding. Axon repulsion in
 CC growth cones may be caused by its association with DCC that may
 CC trigger signaling for repulsion. It also acts as a dependence
 CC receptor required for apoptosis induction when not associated with
 CC netrin ligand (By similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q6UXZ4-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q6UXZ4-2; Sequence=VSP_011703;
 CC Note=No experimental confirmation available;
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AB055056; BAB83663.1; -.
 DR EMBL; AY358147; AAQ88514.1; -.
 DR HSSP; P07996; 1LSL.
 DR Genew; HGNC:18634; UNC5D.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.

DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 953 Netrin receptor UNC5D.
 FT DOMAIN 33 379 Extracellular (Potential).
 FT TRANSMEM 380 400 Potential.
 FT DOMAIN 401 953 Cytoplasmic (Potential).
 FT DOMAIN 54 151 Ig-like.
 FT DOMAIN 153 244 Ig-like C2-type.
 FT DOMAIN 252 306 TSP type-1 1.
 FT DOMAIN 308 360 TSP type-1 2.
 FT DOMAIN 540 642 ZU5.
 FT DOMAIN 859 936 Death.
 FT SITE 416 417 Cleavage (by caspase-3) (By similarity).
 FT SITE 703 721 Interaction with DCC (By similarity).
 FT DISULFID 75 134 By similarity.
 FT DISULFID 180 231 By similarity.
 FT CARBOHYD 117 117 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 228 228 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 353 353 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 376 376 N-linked (GlcNAc. . .) (Potential).
 FT VARSPLIC 1 34 MGRAAATAGGGGGGARRWLPWLGLCFWAAGTAAAR -> MIL
 FT VLVKALSDVCAGTSGFLLDFFSSQTSP (in isoform
 FT 2).
 FT /FTId=VSP_011703.
 SQ SEQUENCE 953 AA; 105879 MW; 5F893B9DF746F731 CRC64;

Query Match 61.7%; Score 201; DB 1; Length 953;
 Best Local Similarity 58.6%; Pred. No. 3e-15;
 Matches 34; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 4 IVLPCRPPGEGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCVA 61
 ||| |||||:| |||||:|: :| | |: :|:|:| |||||:|: ||||:|
 Db 176 IVLHCRPPEGVPAAEVEWLKNEEPIDSEQDENIDTRADHNLIIRQARLSDSGNYTCMA 233

RESULT 14

UN5D_MOUSE

ID UN5D_MOUSE STANDARD; PRT; 956 AA.
 AC Q8K1S2;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4).
 GN Name=Unc5d; Synonyms=Unc5h4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
 RA Engelkamp D.;
 RT "Cloning of three mouse Unc5 genes and their expression patterns at
 RT mid-gestation.";
 RL Mech. Dev. 118:191-197(2002).
 CC -!- FUNCTION: Receptor for netrin involved in cell migration. May be
 CC involved in axon guidance by mediating axon repulsion of neuronal
 CC growth cones in the developing nervous system upon ligand binding.
 CC Axon repulsion in growth cones may be caused by its association
 CC with DCC that may trigger signaling for repulsion. It also acts as
 CC a dependence receptor required for apoptosis induction when not
 CC associated with netrin ligand (By similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in developing limb and mammary
 CC gland.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AJ487854; CAD32252.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:2389364; Unc5d.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.

DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 30 Potential.
 FT CHAIN 31 956 Netrin receptor UNC5D.
 FT DOMAIN 31 382 Extracellular (Potential).
 FT TRANSMEM 383 403 Potential.
 FT DOMAIN 404 956 Cytoplasmic (Potential).
 FT DOMAIN 52 149 Ig-like.
 FT DOMAIN 151 242 Ig-like C2-type.
 FT DOMAIN 250 304 TSP type-1 1.
 FT DOMAIN 306 358 TSP type-1 2.
 FT DOMAIN 543 645 ZU5.
 FT DOMAIN 862 939 Death.
 FT SITE 419 420 Cleavage (by caspase-3) (By similarity).
 FT SITE 706 724 Interaction with DCC (By similarity).
 FT DISULFID 73 132 By similarity.
 FT DISULFID 178 229 By similarity.
 FT CARBOHYD 115 115 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 226 226 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 351 351 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 379 379 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 956 AA; 106351 MW; DFDF07839C10C68D CRC64;

Query Match 61.7%; Score 201; DB 1; Length 956;
 Best Local Similarity 58.6%; Pred. No. 3e-15;
 Matches 34; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 4 IVLPCRPPGIPPAEVEWLRNEDLVDPSPNVYITREHSLVVRQARLADTANYTCVA 61
 ||| |||||:| |||||:|:| | | : |:|:|:|||||:|: ||||:|
 Db 174 IVLHCRPPGVPAAEVEWLKNEEPIDSEQDENIDTRADHNLIRQARLSDSGNYTCMA 231

RESULT 15

UNC5_CAEEL

ID UNC5_CAEEL STANDARD; PRT; 919 AA.
 AC Q26261; O44171; Q26262; Q7JPT6; Q7KPX0;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor unc-5 precursor (Uncoordinated protein 5).
 GN Name=unc-5; ORFNames=B0273.4;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B), AND FUNCTION.
 RX MEDLINE=93046629; PubMed=1384987; DOI=10.1016/0092-8674(92)90357-I;
 RA Leung-Hagesteijn C., Spence A.M., Stern B.D., Zhou Y., Su M.-W.,
 RA Hedgecock E.M., Culotti J.G.;
 RT "UNC-5, a transmembrane protein with immunoglobulin and thrombospondin
 RT type 1 domains, guides cell and pioneer axon migrations in C.

RT elegans.";
 RL Cell 71:289-299(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [3]
 RP REVISIONS, AND ALTERNATIVE SPLICING.
 RA Waterston R.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP FUNCTION.
 RX PubMed=8332188; DOI=10.1038/364327a0;
 RA Hamelin M., Zhou Y., Su M.-W., Scott I.M., Culotti J.G.;
 RT "Expression of the UNC-5 guidance receptor in the touch neurons of C.
 RT elegans steers their axons dorsally.";
 RL Nature 364:327-330(1993).
 RN [5]
 RP FUNCTION.
 RX PubMed=10631179;
 RA Su M.-W., Merz D.C., Killeen M.T., Zhou Y., Zheng H., Kramer J.M.,
 RA Hedgecock E.M., Culotti J.G.;
 RT "Regulation of the UNC-5 netrin receptor initiates the first
 RT reorientation of migrating distal tip cells in Caenorhabditis
 RT elegans.";
 RL Development 127:585-594(2000).
 RN [6]
 RP FUNCTION.
 RX PubMed=11454756;
 RA Merz D.C., Zheng H., Killeen M.T., Krizus A., Culotti J.G.;
 RT "Multiple signaling mechanisms of the UNC-6/netrin receptors UNC-5 and
 RT UNC-40/DCC in vivo.";
 RL Genetics 158:1071-1080(2001).
 RN [7]
 RP PHOSPHORYLATION.
 RX PubMed=11533026; DOI=10.1074/jbc.M103872200;
 RA Tong J., Killeen M., Steven R., Binns K.L., Culotti J., Pawson T.;
 RT "Netrin stimulates tyrosine phosphorylation of the UNC-5 family of
 RT netrin receptors and induces Shp2 binding to the RCM cytodomain.";
 RL J. Biol. Chem. 276:40917-40925(2001).
 RN [8]
 RP PHOSPHORYLATION SITE TYR-482, TISSUE SPECIFICITY, MUTANT EV585, AND
 RP MUTAGENESIS OF 387-TYR-TYR-388; TYR-417; TYR-439; TYR-482; TYR-538 AND
 RP TYR-691.
 RX PubMed=12435363;
 RA Killeen M., Tong J., Krizus A., Steven R., Scott I., Pawson T.,
 RA Culotti J.;
 RT "UNC-5 function requires phosphorylation of cytoplasmic tyrosine 482,
 RT but its UNC-40-independent functions also require a region between the
 RT ZU-5 and death domains.";
 RL Dev. Biol. 251:348-366(2002).
 CC -!- FUNCTION: Receptor for netrin (unc-6) required for axon guidance.
 CC Mediates axon repulsion of neuronal growth cones in the developing

nervous system upon ligand binding. Axon migration is mediated by the secreted unc-6, which promotes attraction of neurons and axons through binding to the unc-40 receptor, while repulsion requires both unc-5 and unc-40 receptors. Also involved in the ventral-to-dorsal migration of the hermaphrodite distal tip cells along the body.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=b;
CC IsoId=Q26261-1; Sequence=Displayed;
CC Name=a;
CC IsoId=Q26261-2; Sequence=VSP_011704;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Expressed in cell bodies and axons of the VNC motor neurons that extend axons to the dorsal midline and within the ventral nerve cord.
CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues. Tyrosine phosphorylation is unc-6-dependent.
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC -!- CAUTION: In contrast to other members of the family, it lacks a canonical signal sequence; the existence of the signal sequence is therefore unsure.

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CC -----

DR EMBL; S47168; AAB23866.2; -.
DR EMBL; S47135; AAB23866.2; JOINED.
DR EMBL; S47136; AAB23866.2; JOINED.
DR EMBL; S47137; AAB23866.2; JOINED.
DR EMBL; S47164; AAB23866.2; JOINED.
DR EMBL; S47165; AAB23866.2; JOINED.
DR EMBL; S47166; AAB23866.2; JOINED.
DR EMBL; S47167; AAB23866.2; JOINED.
DR EMBL; S47168; AAB23867.2; -.
DR EMBL; S47134; AAB23867.2; JOINED.
DR EMBL; S47135; AAB23867.2; JOINED.
DR EMBL; S47136; AAB23867.2; JOINED.
DR EMBL; S47137; AAB23867.2; JOINED.
DR EMBL; S47164; AAB23867.2; JOINED.
DR EMBL; S47165; AAB23867.2; JOINED.
DR EMBL; S47166; AAB23867.2; JOINED.
DR EMBL; S47167; AAB23867.2; JOINED.
DR EMBL; AF036698; AAB88355.1; -.
DR EMBL; AF036698; AAB88356.1; -.
DR PIR; B44294; B44294.

DR PIR; T32541; T32541.
 DR HSSP; P07996; 1LSL.
 DR WormBase; WBGene00006745; unc-5.
 DR WormPep; B0273.4a; CE16790.
 DR WormPep; B0273.4b; CE16791.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 ? Potential.
 FT CHAIN ? 919 Netrin receptor unc-5.
 FT DOMAIN ? 340 Extracellular (Potential).
 FT TRANSMEM 341 361 Potential.
 FT DOMAIN 362 919 Cytoplasmic (Potential).
 FT DOMAIN 15 113 Ig-like.
 FT DOMAIN 111 198 Ig-like C2-type.
 FT DOMAIN 202 272 TSP type-1 1.
 FT DOMAIN 274 326 TSP type-1 2.
 FT DOMAIN 500 609 ZU5.
 FT DOMAIN 829 910 Death.
 FT DISULFID 25 84 By similarity.
 FT DISULFID 132 181 By similarity.
 FT MOD_RES 482 482 Phosphotyrosine.
 FT CARBOHYD 178 178 N-linked (GlcNAc. . .) (Potential).
 FT VARSPLIC 1 1 M -> MEDDTPDVSSDSNGDAAYSDYFLDYKSIM (in
 FT isoform a).
 FT /FTId=VSP_011704.
 FT MUTAGEN 181 181 C->Y: In ev585; temperature sensitive
 FT allele leading to distal tip cells
 FT migration defects.
 FT MUTAGEN 387 388 YY->FF: Induces a strong decrease in
 FT tyrosine phosphorylation but only weakly
 FT affects function in vivo; when associated
 FT with F-417, F-439, F-538 and F-691.
 FT MUTAGEN 417 417 Y->F: Induces a strong decrease in
 FT tyrosine phosphorylation but only weakly
 FT affects function in vivo; when associated
 FT with F-387, F-388, F-439, F-538 and F-
 FT 691.
 FT MUTAGEN 439 439 Y->F: Induces a strong decrease in
 FT tyrosine phosphorylation but only weakly
 FT affects function in vivo; when associated

FT				with F-387, F-388, F-417, F-538 and F-691.
FT				
FT	MUTAGEN	482	482	Y->F: Loss of function and induces a strong decrease in tyrosine phosphorylation.
FT				
FT	MUTAGEN	538	538	Y->F: Induces a strong decrease in tyrosine phosphorylation but only weakly affects function in vivo; when associated with F-387, F-388, F-417, F-439 and F-691.
FT				
FT				
FT	MUTAGEN	691	691	Y->F: Induces a strong decrease in

Query Match 37.7%; Score 123; DB 1; Length 919;
 Best Local Similarity 44.6%; Pred. No. 7.7e-06;
 Matches 25; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

Qy	6	LPCRPPGIPPAEVEWLRNEDLVDPSPDPNVYITREHSLVVRQARLADTANYTCVA	61
		: : :: : : :: : :	
Db	130	LPCQAPESDPKAELTWYKDGVVVQP--DANVIRASDGS LIMSAARLSDSGNYTCEA	183

Search completed: March 1, 2005, 09:03:35
 Job time : 13.1589 secs